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Remarks:
- The applicant has subsequently filed a sequence listing and declared, that it includes no new matter.
- Claims 11 to 12 are deemed to be abandoned due to non-payment of the claims fees (Rule 31 (2) EPC).

(54) Gastric helicobacter 16 S rDNA sequences from cattle and pigs and their use for detection and typing of Helicobacter strains

(57) The present invention relates to new *Helicobacter* 16S rRNA or rDNA polynucleotide sequences useful for detection and typing of *Helicobacter* infected human and animal samples. The present invention relates more particularly to new "*Candidatus* Helicobacter bovis" and "*Candidatus* Helicobacter suis" sequences as defined in SEQ ID NO 1 and 2, sequence variants and fragments thereof. These new *Helicobacter* sequences allow the design of sequence specific probes and primers for detection and typing of the strains they are derived from. Diagnostic methods and kits employing such new bovine and porcine *Helicobacter* sequences are also disclosed.

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Description

[0001] The present invention relates to the field of detection and typing of *Helicobacter* infection in clinical samples from humans and other mammals. The present invention relates more particularly to bovine and porcine 16 rDNA polynucleotide sequences as well as their use in diagnostic applications.

[0002] In the 19th century, gastric spiral organisms were described for the first time in different animals (Rappin, 1881; Bizzozero, 1893; Salomon, 1896). Salomon observed spiral organisms in the stomachs of dogs, cats and the brown Norwegian rat but not in humans, monkeys, pigs, mice, pigeons, crows and cattle (Salomon, 1896). It was only in 1984 that a renewed interest emerged for similar organisms after the isolation of *Helicobacter pylori* from the human stomach (Marshall & Warren, 1984). The association of *H. pylori* with chronic gastrilis, peptic ulceration and gastric cancer (Cover & Blaser, 1992; Blaser et al., 1991; Parsonnet et al., 1991) resulted in intensive research worldwide. Various *Helicobacter* species were isolated from the gastrointestinal tract of different animals. To date, the genus *Helicobacter* consists of 18 different species (On, 1996; Franklin et al., 1996; Mendes et al., 1996; Jalava et al., 1997; Trivett-Moore et al., 1997; Shen et al., 1997) and constitutes together with the genera *Wolinella, Campylobacter* and *Arcobacter,* the epsilon subdivision of the *Proteobacteria*, also known as rRNA superfamily VI (Vandamme et al., 1991).

[0003] In 1992, two different groups almost simultaneously reported the presence of helically shaped bacteria in the abomasum of calves and adult cattle based on histological data (Günther & Schulze, 1992; Haringsma & Mouwen, 1992). Both groups described large numbers of spiral-shaped bacteria in the gastric crypts of the pyloric region and considered them as putative *Helicobacter* species. Further indirect evidence of the presence of *Helicobacter-like* organisms in adult cattle and calves was given by serological studies. Seidel et al. (1996) found significant titers of antibodies against H. *pylori* epitopes in the serum of calves after absorption with *Campylobucter jejuni, Wolinella succinogenes, Escherichia coli* and *Proteus mirabilis* strains. One report described a bactericidal activity of bovine serum, colostrum and milk against *H. pylori* (Korhonen et al., 1995). In vitro isolation of these organisms has not been successful so far (Jelinski et al., 1995; Braun et al., 1997) and the taxonomic status of these putative *Helicobacter*-like bacteria is unknown.

[0004] The pathogenic role of *H. pylori* led to speculations about the association of bovine *Helicobacter*-like bacteria with abomasal ulcer disease, although no conclusive evidence has been provided to date (Günther & Schulze, 1992; Haringsma & Mouwen, 1992). Other bacteria such as *Campylobacter* species and *Clostridium perfringens* have also been studied in association with the occurrence of abomasal lesions (Al Mashat & Taylor, 1980; Mills et al., 1990, Jelinski et al., 1995).

[0005] Within the genus *Helicobacter,* a phylogenetic subgroup of morphologically similar bacteria can be distinguished. These bacteria, characterized by their long and tightly coiled (gastrospirillum-like) appearance, have been observed in gastric biopsies of humans, cats, lemurs, dogs, pigs and exotic carnivores (Dent et al., 1987; Lee et al., 1988; O'Rourke et al., 1992; Hänninen et al., 1996; Jalava et al., 1997; Queiroz et al., 1990; Eaton et al., 1993; Jakob et al., 1997). Three species with this morphology (*H. felis, H. bizzozeronii, H. salomonis)* have been isolated and characterised from gastric samples of cats and dogs (Paster et al., 1991; Hänninen et al., 1996; Jalava et al., 1997).

[0006] The observation of gastrospirillum-like organisms in humans was described for the first time in 1987 by Dent et al (Dent et al., 1987). Although initially referred to as "*Gastrospirillum hominis*" (McNulty et al., 1989), this organism was later renamed "*Helicobacter heilmannii*" as 16S rDNA sequence analysis revealed that these human gastrospirilla belonged to the genus *Helicobacter* (O'Rourke et al., 1992; Solnick et al., 1993). From these results, it also became clear that there were at least two different types of "*Helicobacter heilmannii*", referred to as type 1 and type 2. This observation was based on a 3.5 % sequence difference, suggesting that the two sequences represented two different species. The first isolation of a "*Helicobacter heilmannii*" - like bacterium from humans was recently reported by Andersen *et al.* (1996).

[0007] In pigs, gastrospirillum-like bacteria were observed in the antral pits and at the mucosal surface of the stomach (Queiroz et al.,1990) and have provisionally been named "*Gastrospirillum suis*" (Mendes et al., 1990). Histopathological studies associated this bacterium with pyloric lymphonodular gastritis (Mendes et al., 1991) and gastric ulcer disease of the pars oesophagea in pigs (Barbosa et al., 1995, Quieroz et al., 1996). Although *in vitro* cultivation of "*Gastrospirillum suis*" has been unsuccessful (Queiroz et al., 1990), *in vivo* cultivation in mice and rats has been reported (Moura et al., 1993; Mendes et al., 1996). In one case, a *Helicobacter* was isolated from the faeces of swine (Seymour et al., 1994) which was later characterised as *Helicobacter pametensis* (Dewhirst et al., 1994). Other members of rRNA superfamily VI, *Campylobacter hyointestinalis* subsp. *Lawsonii* (On et al., 1995), *Arcobacter butzleri* and *Arcobacter cryaerophilus* (Suarez et al., 1997), have also been isolated from the stomach of swine.

[0008] As "*Gastrospirillum suis*" remains unculturable, an official species designation is impossible according to the guidelines of the *International Code of Nomenclature of Bacteria* which are stating the necessity of a broad range of phenotypic and phylogenetic data. Murray and Schleifer (1994) anticipated this problem, and proposed a provisional status to record the properties of putative taxa of prokaryotes. This proposal was implemented in 1995 by the International Committee on Systematic Bacteriology by the introduction of the provisional status *Candidatus* for the description

of uncultivable organisms based upon genomic data and to a certain extent structural, metabolic, reproductive and environmental characteristics (Murray and Stackebrandt, 1995).

[0009] It is an aim of the present invention to provide new *Helicobacter* nucleotide sequences of the 16S rRNA coding gene.

[0010] It is also an aim of the present invention to provide new probes and primers for detection of *Helicobacter* species.

[0011] It is also an aim of the present invention to provide methods and kits for detection and/or typing of *Helicobacter* species present in cattle and pigs.

[0012] It is further an aim of the present invention to provide methods and kits for detection of zoönoses in human samples.

[0013] It is also an aim of the present invention to provide new nucleotide sequences for studying and detecting the occurrence of pathogenic *Helicobacter* strains in mammals, more particularly in cattle and pigs.

[0014] All the aims of the present invention are met by the following embodiments.

[0015] According to one embodiment, the present invention relates to an isolated 16S rDNA *Helicobacter* polynucleic acid sequence selected from any of the following

(a) a sequence represented in any of SEQ ID NO 1 or 2, or the RNA version thereof,

(b) a sequence which hybridizes under stringent conditions to any of the sequences set out in (a).

[0016] The term "16S ribosomal polynucleic acid sequences" as used in the present invention refers to 16S rRNA or 16S rDNA polynucleic acid sequences.

[0017] According to a first aspect of the present invention, seven abomasal biopsies of adult cattle were sampled from different Belgian and Dutch farms. In all samples the presence of *Helicobacter*-like organisms was demonstrated by biochemical, immunohistochemical and electronmicroscopical data. Bacterial 16S rDNA was amplified from each sample by PCR and sequences were determined either by direct or indirect sequence analysis. Pairwise comparisons revealed all sequences to be more than 99 % homologous. Phylogenetic analysis placed the organism, corresponding to the reference sequence R2XA, within the genus *Helicobacter*. A diagnostic PCR-assay was designed, differentiating the bovine 16S rDNA sequences from those of 15 different *Helicobacter* strains and *Wolinella succinogenes*. These results indicated the corresponding organism to represent a single taxon. The low similarity level towards *H. bilis* (92.8 %), its closest validly named neighbour, strongly suggests that this novel taxon indeed is a novel *Helicobacter* species. An *in situ* hybridisation procedure associated the bovine sequences to the *Helicobacter*-like organisms in the abomasum.

[0018] According to a second aspect, the present invention relates to new *Helicobacter* sequences from pigs. Stomachs of five slaughterhouse pigs originating from different Belgian and Dutch farms were selected based on the presence of *"Gastrospirillum suis"*-like bacteria as demonstrated by biochemical, immunohistochemical and electronmicroscopical data. Using broad range primers, bacterial 16S rDNA was amplified by PCR and five *Helicobacter*-like sequences were determined either by direct or indirect sequence analysis. An intersequence homology of 99.7 % was observed, suggesting that the sequences originated from strains belonging to a single species. Phylogenetic analysis of the consensus sequence placed the organism within the genus *Helicobacter,* where it formed a distinct subgroup together with other gastrospirillum-like bacteria *(H. felis, H. bizzozeronii, H. salomonis, "H heilmannii"* type 1 and type 2). Diagnostic PCR-primers and a probe were developed, differentiating the porcine sequences from all known *Helicobacters*. These results indicate that the porcine sequences represent a single taxon within the genus *Helicobacter.* The low similarity level towards *H. salomonis* (96.6 %), its closest validly named neighbour, strongly suggests that this novel taxon indeed is a novel *Helicobacter* species. *In situ* hybridisation experiments linked the reference sequence to the *"Gastrospirillum suis"*-like bacteria. On the basis of these results, the name *"Candidatus* Helicobacter suis" for this new gastric *Helicobacter* from pigs is proposed.

[0019] These sequences are commonly characterized by the fact that they can be used to study and most probably detect pathogenic *Helicobacter* strains in mammals, more particularly in cattle and pigs. Such pathogenic strains cause for instance gastric ulcers and chronic gastritis.

[0020] The present invention relates more particularly to an isolated polynucleic acid sequence as defined above represented by any of SEQ ID NO 1 or 2 or 15 to 24.

[0021] The present invention also relates to an isolated polynluceic acid sequence as defined above which is more than 92.8%, preferably more than 93.5%, more preferably more than 95% and most preferably more than 97.5% homologous to SEQ ID NO 1. Other preferred ranges of homology include 93, 94, 94.5, 95.5, 96, 96.5, 97, 98, 98.5, 99 or 99.5%.

[0022] Sequences which have a homology of more than 92.8% to SEQ ID NO 1 are considered to belong to the same group of organisms as the one where SEQ ID NO 1 has been derived from.

[0023] According to the present invention, the homologies of SEQ ID NO 1 were calculated by means of the GENESCAN program (Applied Maths bvba, Risquons-toutstraat 38, B-8511 Kortrijk, Belgium).

[0024] The term "homology" refers to a sequence identity as calculated by the above-given program.

[0025] SEQ ID NO 2 is 99.5% homologous to the closest found sequence. Sequences of more than 99.5% homology compared to SEQ ID NO 2 are also within the scope of the present invention.

[0026] Preferred sequences according to the present invention are set out in Figures 1, 2, 4 and 5: SEQ ID NO 1 to 2 and 15 to 24. Also unique parts and fragments of these sequences are part of the present invention. Preferred unique parts are set out in Table 2.

[0027] Since SEQ ID NO 2 shows 96.6% homology to its closest found validly named neighbour, the use of sequences of more than 96.6% homology to SEQ ID NO 1 for identification or typing of *Helicobacter* species is also within the scope of the present invention. Preferably sequences of more than 97%, 97.5%, 98%, 98.5%, 99% or 99.5% homology to SEQ ID NO 2 are used for this goal.

[0028] According to another embodiment, the present invention relates to a part of an isolated polynucleic acid as defined above, more particularly part or a fragment of SEQ ID NO 1 or 2, wherein said part is unique to the polynucleic acid sequence it is derived from.

[0029] According to the present invention, the term "unique" implies that at least one nucleotide of the fragment or part is different from a nucleotide present at the same nucleotide position in a known 16S rRNA sequence or the corresponding gene. Such a nucleotide can be deduced theoretically by looking at an alignment of the new sequences of this invention with other closely related *Helicobacter* 16S rDNA gene nucleotide sequences (see Figures 1, 2, 4 and 5). Said type of nucleotides are unique to the sequence they are derived from. These fragments are thus not part of any known 16S rRNA or gene sequence encoding the same. The fragments according to this embodiment of the present invention may be of any length between 10 to the maximum number of nucleotides of SEQ ID NO 1 or 2 or its variants. Preferred lengths are 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, etc. nucleotides.

[0030] According to another embodiment, the present invention relates to a probe which specifically hybridizes to a polynucleic acid sequence as defined above.

[0031] Preferred probes are given in Table 2. Probe *R628f* is a preferred "*Candidatus* Helicobacter bovis" specific probe. Probe *V100f* is a preferred "*Candidatus* Helicobacter suis" specific probe. Other suitable probes may be derived from a visual inspection of the alignment shown in Figure 1 or 2.

[0032] According to another embodiment, the present invention relates to a primer which specifically amplifies a polynucleic acid sequence as defined above.

[0033] Preferred primers according to the present invention are given in Table 2. Primers *R574f and R832r* are preferred "*Candidatus* Helicobacter bovis" specific primers and are suited for a specific PCR and in situ hybridisation assays. Primers *V832f* and *V1621r* are preferred "*Candidatus* Helicobacter suis" specific primers for a specific PCR and in situ hybridisation assays. Other suitable primers according to the present invention may be derived from a visual inspection of the alignment shown in Figure 1 or 2.

[0034] Relying on the principles well kown in the art, the skilled man will be able to select primers that allow specific amplification of SEQ ID NO 1 or 2 or the claimed variants thereof under given or experimental conditions, such as temperature, buffer composition, polymerase chain reaction cycle etc. Likewise the skilled man will be able to select probes that specifically hybridize to either SEQ ID NO 1 or 2 or the claimed variants under given experimental conditions such as temperature, buffer composition etc. Having chosen primers and/or probes, the skilled man will furthermore be able to assess the efficacy of these primers or probes without undue experimentation. It is also obvious that the skilled man may chose to combine more than one primer pair or more than one probe to carry out the method defined above.

[0035] In some cases, one may not wish to detect all SEQ ID NO 1 or 2 variants as specified above, for instance if one intends to detect alleles found in a certain geographic region.

[0036] According to another embodiment, the present invention relates to a method for detection and/or typing of *Helicobacter* strains present in a biological sample comprising hybridizing the 16S rRNA or 16S rDNA target region polynucleotides of said *Helicobacter* strains present in said biological sample with at least one probe as defined above.

[0037] Preferably said method may be used to study and detect the occurrence of pathogenic *Helicobacter* strains.

[0038] According to another embodiment, the present invention relates to a method for detection and/or typing of *Helicobacter* strains present in a biological sample comprising specifically amplifying the 16S rRNA or 16S rDNA target region polynucleotides of said *Helicobacter* strains present in said biological sample with at least one primer as defined above.

[0039] Preferably said method may be used to study and detect the occurrence of pathogenic *Helicobacter* strains.

[0040] A preferred embodiment according to the present invention involves a method for detection and/or typing of *Helicobacter* strains present in a biological sample comprising first amplifying a specifc target region encompassed in or comprising the 16S rRNA region of said *Helicobacter* strains present in said biological sample and subsequently hybridizing the 16S rRNA or 16S rDNA target region polynucleotides of said *Helicobacter* strains present in said bio-

logical sample with at least one (or more than one) probe as defined above.

[0041] Different techniques can be applied to perform the methods of the present invention. These techniques may comprise immobilizing the target polynucleic acids, possibly after amplification, on a solid support and performing a hybridization with labelled oligonucleotide probes of the present invention. Alternatively, said probes may be immobilized on a solid support and hybridization may be performed with labelled target polynucleic acids, possibly after amplification (i.e. a reverse hybridization).

[0042] A preferred method according to the present invention is an *in situ* hybridisation assay (see Examples section).

[0043] The well-known technique of Southern blotting is one example of a hybridization assay that can be used to perform the methods of the present invention. Another example of a hybridization technique is the DNA enzyme immuno assay (DEIA). According to this method, PCR products are generated by a primer set, of which either the forward or the reverse primer contain biotin at the 5' end. This allows binding of the biotinylated amplimers to streptavidin-coated microtiter wells. PCR products are denatured by sodium hydroxide, which allows removal of the non-biotinylated strand. Specific digoxigenin (DIG)-labelled oligonucleotide probes are hybridized to the single-stranded immobilized PCR product and hybrids are detected by enzyme-labelled conjugate and colorimetric methods.

[0044] A convenient reverse hybridization technique is the LiPA assay. The LiPA uses oligonucleotide probes immobilized as parallel lines on a solid support strip (Stuyver et al. 1993; international patent application WO 94/12670). This approach is particularly advantageous since it is fast and simple to perform.

[0045] It is to be understood that any other type of hybridization assay or hybridization format using any of the selected probes as described further in the invention, is also covered by the present invention.

[0046] According to another embodiment , the present invention relates to a diagnostic kit for detection and/or typing of *Helicobacter* strains comprising:

- at least one probe as defined above and/or,
- at least one primer as defined above.

[0047] According to another embodiment, the present invention relates to a medicament comprising a polynucleic acid sequence as defined above.

[0048] According to another embodiment, the present invention relates to a polynucleic acid sequence as defined above for use as a medicament.

[0049] The following definitions and explanations will permit a better understanding of the present invention.

[0050] The target material in the samples to be analysed may either be DNA or RNA, e.g. genomic DNA, messenger RNA, viral RNA or amplified versions thereof. These molecules are in this application also termed "polynucleic acids" or "polynucleotides". More particularly, the target material according to the present invention will be 16S ribosomal RNA or DNA or amplified versions thereof.

[0051] Well-known extraction and purification procedures are available for the isolation of RNA or DNA from a sample (e.g. in Sambrook et al.,1989).

[0052] The term "probe" according to the present invention refers to a single-stranded oligonucleotide which is designed to specifically hybridize to "*Candidatus* Helicobacter bovis or suis" polynucleic acids.

[0053] The term "primer" refers to a single stranded oligonucleotide sequence capable of acting as a point of initiation for synthesis of a primer extension product which is complementary to the nucleic acid strand to be copied. The length and the sequence of the primer must be such that they allow to prime the synthesis of the extension products. Preferably the primer is about 5-50 nucleotides long. Specific length and sequence will depend on the complexity of the required DNA or RNA targets, as well as on the conditions at which the primer is used, such as temperature and ionic strength. It is to be understood that the primers of the present invention may be used as probes and *vice versa*, provided that the experimental conditions are adapted.

[0054] The expression "suitable primer pair" in this invention refers to a pair of primers allowing specific amplification of a "*Candidatus* Helicobacter bovis or suis" polynucleic acid fragment.

[0055] The term "target region" of a probe or a primer according to the present invention is a sequence within the "*Candidatus* Helicobacter bovis or suis" polynucleic acids to which the probe or the primer is completely complementary or partially complementary (i.e. with some degree of mismatch). It is to be understood that the complement of said target sequence is also a suitable target sequence in some cases.

[0056] "Specific hybridization" of a probe to a target region of respectively the "*Candidatus* Helicobacter bovis" or *Candidatus* Helicobacter suis" polynucleic acids means that said probe forms a duplex with part of this region or with the entire region under the experimental conditions used, and that under those conditions said probe does not form a duplex with other regions of the polynucleic acids present in the sample to be analysed.

[0057] "Specific hybridization" of a primer to a target region of respectively the "*Candidatus* Helicobacter bovis" or "*Candidatus* Helicobacter suis" polynucleic acids means that, during the amplification step, said primer forms a duplex

with part of this region or with the entire region under the experimental conditions used, and that under those conditions said primer does not form a duplex with other regions of the polynucleic acids present in the sample to be analysed. It is to be understood that "duplex" as used hereby, means a duplex that will lead to specific amplification.

[0058] "Specific amplification" of a fragment of respectively the "*Candidatus* Helicobacter bovis" or *Candidatus* Helicobacter suis" polynucleic acids means amplification of the fragment for which the primers were designed, and not of any other fragment of the polynucleic acids present in a sample.

[0059] The fact that amplification primers do not have to match exactly with the corresponding target sequence in the template to warrant proper amplification is amply documented in the literature (Kwok et al., 1990). However, when the primers are not completely complementary to their target sequence, it should be taken into account that the amplified fragments will have the sequence of the primers and not of the target sequence. Primers may be labelled with a label of choice (e.g. biotine). The amplification method used can be either polymerase chain reaction (PCR; Saiki et al., 1988), ligase chain reaction (LCR; Landgren et al., 1988; Wu & Wallace, 1989; Barany, 1991), nucleic acid sequence-based amplification (NASBA; Guatelli et al., 1990; Compton, 1991), transcription-based amplification system (TAS; Kwoh et al., 1989), strand displacement amplification (SDA; Duck, 1990) or amplification by means of Qß replicase (Lomeli et al., 1989) or any other suitable method to amplify nucleic acid molecules known in the art.

[0060] Preferably, the probes of the invention are about 5 to 50 nucleotides long, more preferably from about 10 to 25 nucleotides. Particularly preferred lengths of probes include 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 or 25 nucleotides. The nucleotides as used in the present invention may be ribonucleotides, deoxyribonucleotides and modified nucleotides such as inosine or nucleotides containing modified groups which do not essentially alter their hybridization characteristics.

[0061] Probe and primer sequences are represented throughout the specification as single stranded DNA oligonucleotides from the 5' to the 3' end. It is obvious to the man skilled in the art that any of the below-specified probes can be used as such, or in their complementary form, or in their RNA form (wherein T is replaced by U).

[0062] The probes according to the invention can be prepared by cloning of recombinant plasmids containing inserts including the corresponding nucleotide sequences, if need be by excision of the latter from the cloned plasmids by use of the adequate nucleases and recovering them, e.g. by fractionation according to molecular weight. The probes according to the present invention can also be synthesized chemically, for instance by the conventional phospho-triester method.

[0063] The oligonucleotides used as primers or probes may also comprise nucleotide analogues such as phosphorothiates (Matsukura et al., 1987), alkylphosphorothiates (Miller et al., 1979) or peptide nucleic acids (Nielsen et al., 1991; Nielsen et al., 1993) or may contain intercalating agents (Asseline et al., 1984). As most other variations or modifications introduced into the original DNA sequences of the invention these variations will necessitate adaptions with respect to the conditions under which the oligonucleotide should be used to obtain the required specificity and sensitivity. However, the eventual results of hybridization will be essentially the same as those obtained with the unmodified oligonucleotides. The introduction of these modifications may be advantageous in order to positively influence characteristics such as hybridization kinetics, reversibility of the hybrid-formation, biological stability of the oligonucleotide molecules, etc.

[0064] The term "solid support" can refer to any substrate to which an oligonucleotide probe can be coupled, provided that it retains its hybridization characteristics and provided that the background level of hybridization remains low. Usually the solid substrate will be a microtiter plate, a membrane (e.g. nylon or nitrocellulose) or a microsphere (bead) or a chip. Prior to application to the membrane or fixation it may be convenient to modify the nucleic acid probe in order to facilitate fixation or improve the hybridization efficiency. Such modifications may encompass homopolymer tailing, coupling with different reactive groups such as aliphatic groups, NH_2 groups, SH groups, carboxylic groups, or coupling with biotin, haptens or proteins.

[0065] The term "labelled" refers to the use of labelled nucleic acids. Labelling may be carried out by the use of labelled nucleotides incorporated during the polymerase step of the amplification such as illustrated by Saiki et al. (1988) or Bej et al. (1990) or labelled primers, or by any other method known to the person skilled in the art. The nature of the label may be isotopic (^{32}P, ^{35}S, etc.) or non-isotopic (biotin, digoxigenin, etc.).

[0066] The "biological sample" may be for instance cultured *Helicobacter* strains, gastric, abomasal stomachs, omasal stomachs, reticulum and rumen, or duodenal biopsies (fresh or parafine material), faeces, saliva, mouth mucosa, gastric juice or urine. Preferably these samples may be taken from piglets, pigs, humans, calves, cattle, etc.

[0067] For designing probes with desired characteristics, the following useful guidelines known to the person skilled in the art can be applied.

[0068] Because the extent and specificity of hybridization reactions such as those described herein are affected by a number of factors, manipulation of one or more of those factors will determine the exact sensitivity and specificity of a particular probe, whether perfectly complementary to its target or not. The importance and effect of various assay conditions are explained further herein.

[0069] **The stability of the [probe : target] nucleic acid hybrid should be chosen to be compatible with the assay

conditions. This may be accomplished by avoiding long AT-rich sequences, by terminating the hybrids with G:C base pairs, and by designing the probe with an appropriate Tm. The beginning and end points of the probe should be chosen so that the length and %GC result in a Tm about 2-10EC higher than the temperature at which the final assay will be performed. The base composition of the probe is significant because G-C base pairs exhibit greater thermal stability as compared to A-T base pairs due to additional hydrogen bonding. Thus, hybridization involving complementary nucleic acids of higher G-C content will be more stable at higher temperatures.

[0070] **Conditions such as ionic strength and incubation temperature under which a probe will be used should also be taken into account when designing a probe. It is known that the degree of hybridization will increase as the ionic strength of the reaction mixture increases, and that the thermal stability of the hybrids will increase with increasing ionic strength. On the other hand, chemical reagents, such as formamide, urea, DMSO and alcohols, which disrupt hydrogen bonds, will increase the stringency of hybridization. Destabilization of the hydrogen bonds by such reagents can greatly reduce the Tm. In general, optimal hybridization for synthetic oligonucleotide probes of about 10-50 bases in length occurs approximately SEC below the melting temperature for a given duplex. Incubation at temperatures below the optimum may allow mismatched base sequences to hybridize and can therefore result in reduced specificity.

[0071] **It is desirable to have probes which hybridize only under conditions of high stringency. Under high stringency conditions only highly complementary nucleic acid hybrids will form; hybrids without a sufficient degree of complementarity will not form. Accordingly, the stringency of the assay conditions determines the amount of complementarity needed between two nucleic acid strands forming a hybrid. The degree of stringency is chosen such as to maximize the difference in stability between the hybrid formed with the target and the non-target nucleic acid.

[0072] **Regions in the target DNA or RNA which are known to form strong internal structures inhibitory to hybridization are less preferred. Likewise, probes with extensive self-complementarity should be avoided. As explained above, hybridization is the association of two single strands of complementary nucleic acids to form a hydrogen bonded double strand. It is implicit that if one of the two strands is wholly or partially involved in a hybrid that it will be less able to participate in formation of a new hybrid. There can be intramolecular and intermolecular hybrids formed within the molecules of one type of probe if there is sufficient self complementarity. Such structures can be avoided through careful probe design. By designing a probe so that a substantial portion of the sequence of interest is single stranded, the rate and extent of hybridization may be greatly increased. Computer programs are available to search for this type of interaction. However, in certain instances, it may not be possible to avoid this type of interaction.

[0073] **Standard hybridization and wash conditions are disclosed in the Examples section. Other conditions are for instance 3X SSC (Sodium Saline Citrate), 20% deionized FA (Formamide) at 50EC. Other solutions (SSPE (Sodium saline phosphate EDTA), TMAC (Tetramethyl ammonium Chloride), etc.) and temperatures can also be used provided that the specificity and sensitivity of the probes is maintained. When needed, slight modifications of the probes in length or in sequence have to be carried out to maintain the specificity and sensitivity required under the given circumstances.

[0074] The term "hybridization buffer" means a buffer allowing a hybridization reaction between the probes and the polynucleic acids present in the sample, or the amplified products, under the appropriate stringency conditions.

[0075] The term "wash solution" means a solution enabling washing of the hybrids formed under the appropriate stringency conditions.

[0076] The Examples as set out below only serve to illustrate the present invention. The contents of all references referred to in this text are hereby incorporated by reference.

FIGURE AND TABLE LEGENDS

[0077]

Figure 1 represents an alignment of the reference sequence R2XA of "*Candidatus* Helicobacter bovis" (SEQ ID NO 1) with sequences of strains belonging to the epsilon subdivision (Table 3) which were retrieved from the EMBL data library and were aligned with reference sequence R2XA

Figure 2 represents an alignment of the reference sequence V2BXA of "*Candidatus* Helicobacter suis" (SEQ ID NO 2) sequence with the sequences of strains belonging to the same phylogenetic lineage (Table 3).

Figure 3A represents a phylogenetic tree based on the phylogenetic analysis of "*Candidates* Helicobacter bovis" as set out in the Examples section. The scale bar represents a one % difference in nucleotide sequences as determined by measuring the length of horizontal lines connecting any two species.

Figure 3B represents a a phylogenetic tree based on the phylogenetic analysis of "*Candidatus* Helicobacter suis" as set out in the Examples section. The scale bar represents a one % difference in nucleotide sequences as determined by measuring the length of horizontal lines connecting any two species.

Figure 4 represents an alignment of the different "*Candidatus* Helicobacter bovis" sequences. The reference sequence is R2XA001 (SEQ ID NO 1). The other sequences are R5XE001 (SEQ ID NO 15), R3XA001 (SEQ ID NO 16), R6XA001 (SEQ ID NO 17), R13D001INV (SEQ ID NO 18), R27TOTAAL (SEQ ID NO 19) and R28TOTAAL (SEQ ID NO 20).

Figure 5 represents an alignment of the different "*Candidatus* Helicobacter suis" sequences. The reference sequence is RBXA001 (SEQ ID NO 2). The other sequences are 4AXA001 (SEQ ID NO 21), 6W06001 (SEQ ID NO 22), V14D001 (SEQ ID NO 23), V19DINV001 (SEQ ID NO 24).

EXAMPLES

Material and Methods

Samples from cattle

[0078] Seven abomasal stomachs from clinically healthy slaughterhouse cattle originating from different Belgian and Dutch farms, were selected. The stomachs were opened longitudinally along the greater curvatura and rinsed gently with tap water. Two small mucosal fragments were taken from each stomach, one near the torus pyloricus and one in the fundic region, and were tested for urease activity (CUTest, Temmler Pharma) for h at 37 °C. Three mucosal biopsies from the pyloric region were taken for immunohistochemistry and *in situ* hybridisation and placed into 4 % buffered formaline for 24 hours. For electronmicroscopy, a pyloric sample was taken from the same region and fixed in cacodylate buffer (0.1 M, pH 7.0) containing 5 % glutaraldehyde and 0.15 % (wt/vol) ruthenium red. From each stomach a mucosal fragment was also taken for PCR analysis, placed into sterile PBS and frozen in liquid nitrogen. Special care was taken during sampling to avoid cross-contamination.

Samples from pigs

[0079] Stomachs from 5 healthy slaughterhouse pigs were selected, all originating from different farms in Belgium and the Netherlands. The stomachs were opened longitudinally along the greater curvatura and rinsed gently with tap water. A small mucosal fragment was taken from each stomach near the torus pyloricus and placed into an urease test tube (CUTest, Temmler Pharma) for 2 hours at 37 °C. Mucosal biopsies from the antral part of the stomach were taken along the curvatura major (n=2) and the curvatura minor (n=2) for immunohistochemical evaluation and placed into 4 % buffered formalin. For electronmicroscopy, samples were taken from the same places and fixed in 0.1 M cacodylate buffer (pH 7.0) containing 5% glutaraldehyde and 0.15 % (wt/vol) ruthenium red. Of each stomach a mucosal fragment was also taken for PCR, placed into sterile PBS and frozen in liquid nitrogen. Special care was taken during sampling to avoid cross-contamination.

Reference strains for "*Candidatus* Helicobacter bovis"

[0080] A total of 15 *Helicobacter* strains and 1 *Wolinella succinogenes* strain were used to test the specificity of the "*Candidatus* Helicobacter bovis" specific PCR (Table 1). Strains were grown on a 5 % Mueller-Hinton blood agar and incubated at 37 °C in a microaerophilic atmosphere containing approximately 5 % O_2, 3.5 % CO_2, 7.5 % H_2 and 84 % N2. Bacteriological purity was checked by plating and Gram-staining.

Reference strains for "*Candidatus* Helicobacter suis"

[0081] A total of 15 *Helicobacter* strains were used to test the specificity of the "*Candidatus* Helicobacter suis"-specific PCR assay (Table 1). Strains were grown on a 5% Mueller-Hinton blood agar and incubated at 37 °C in a microaerobic atmosphere containing approximately 5 % O_2, 3.5 % CO_2, 7.5 % H_2 and 84 % N_2. Bacteriological purity was checked by plating and Gram-staining.

Immunohistochemistry

[0082] Immunohistochemical staining was performed to assess the presence of *Helicobacter*-like organisms. Formalin-fixed samples were dehydrated and paraffin-embedded. Sections of 4 µm were made of the paraffin-embedded tissues and were placed on 3-aminopropyltriethoxysilane-coated slides (APES, Sigma-Aldrich) and dried overnight at 60 °C. After dewaxing with xylene and rehydration in graded series with ethanol and distilled water, sections were placed in citrate buffer (0.1M with 2% ureum) and were boiled (1 x 3 min, 2 x 5 min) in a 800 Watt microwave oven

(Whirlpool M611) to elicit antigen retrieval. Slides were then incubated with 12 % hydrogenperoxide in methanol (30 min) in order to block endogenous peroxidase activity. Thereafter the slides were pre-incubated with 30 % normal goat serum in PBS for 30 min to reduce non-specific antibody binding. A mouse polyclonal antibody directed against *H. pylori* (DAKO), diluted 1/20 in PBS, was incubated overnight at 21 °C in a moist chamber. The sections were washed and incubated with biotinylated swine anti-rabbit immunoglobulins at 21 °C for 30 min and after rinsing covered with peroxidase conjugated streptavidin-biotin-complex (ABC). Peroxidase activity was developed using H_2O_2 with diaminobenzidine (DAB) as a chromogen (Fast DAB Tablet Set, Sigma-Aldrich). Subsequently, the sections were counterstained with Mayer's hematoxylin and mounted. As a negative control, the primary antibody was replaced with fetal calf serum in Tris-HCl buffer (pH 7.6). As a positive control, a section of a mouse stomach experimentally infected with *Helicobacter pylori* LMG 7539^T was used.

Transmission electronmicroscopy

[0083] For "*Candidatus* Helicobacter bovis", three different pyloric samples were selected for electronmicroscopic evaluation based upon the high presence of *Helicobacter*-like organisms in the corresponding immunostained sections.

[0084] For "*Candidatus* Helicobacter suis", two different antral biopsies were selected for electronmicroscopic evaluation based on the high presence of gastrospirillum-like organisms in the corresponding immunostained slides.

[0085] After dehydration in a graded series of acetone washes, the samples were embedded in Spurr low-viscosity resin. Ultrathin sections were poststained with uranyl acetate and lead citrate and examined with an electronmicroscope (Phillips 201 TEM) at an accelerating voltage of 60 kV.

DNA-extraction

[0086] DNA was isolated from the scrapings of the gastric biopsies and from the reference strains by lysis with guanidinium isothiocyanate and DNA was bound to silica particles according to the method of Boom et al. (1990).

Primers and PCR amplification of 16S rDNA

[0087] Broadrange primers *H33f, H61f* and *H1368r* were selected from rRNA superfamily VI *(Helicobacter, Campylobacter, Arcobacter, Wolinella)* specific regions of the 16S rRNA gene (Table 2).

[0088] The use of broad range primer *1492RPL* was suggested by Weissburg et al. (1991). A genus *Helicobacter*-specific primer *H274f* was adapted from primer *274r* described by Dewhirst et al. (1994) (Table 2). Primer combinations *H33F-H1368r, H274f-1492RPL* and *H61f-1492RPL* were used to amplify a ~ 1.3-Kb, ~ 1.2-Kb and a ~1.4-Kb fragment of "*Candidatus* Helicobacter suis" respectively.

[0089] PCR reactions were performed in a volume of 50 µl containing 10mM Tris HCl (pH 8.3), 50 mM KCl, 3.5 mM $MgCl_2$, 200 pM of each deoxynucleoside triphosphate, 1.5 U of AmpliTaq Gold (Perkin-Elmer, Roche Molecular Systems) and 25 pmol of both forward and reverse primer (Eurogentec). Reactions were covered with mineral oil and PCR was performed in a Biomed-60 thermocycler under the following conditions: 9 min preincubation at 94 °C to activate AmpliTaq Gold, followed by 50 cycles of 30 s at 94 °C, 45 s at 55 °C and 45 s at 72 °C. Final extension was performed for 5 min at 72 °C. DNA-extractions of *Helicobacter acinonychis* LMG 12684^T and *Helicobacter mustelae* LMG 8776 were used as positive controls.

Analysis of amplified samples

[0090] PCR products were separated on 1 % agarose gels and stained with ethidium bromide.

[0091] DNA-extractions of *H. acinonychis* LMG 12684^T and *H. mustelae* LMG 8776 were used as positive controls.

[0092] In order to determine whether PCR products were derived from *Helicobacter*-like organisms, the desired DNA-bands were cut from the gels, diluted 1/2 in distilled water and sequenced using the *H33f* and *H1368r* 5'-Indocarbocyanin (Cy5) for "*Candidatus* Helicobacter bovis" and respectively *H61f* and *1492RPL* Indocarbocyanin (Cy5) labeled for "*Candidatus* Helicobacter suis". Partial sequences were screened for homologous sequences using the NCBI GENINFO® BLAST Network service (http://www.ncbi.nlm.nih.gov/BLAST/) (Altshul et al., 1997).

DNA cloning and sequence analysis for "*Candidatus* Helicobacter bovis"

[0093] PCR amplimers comprising the 16S rDNA-sequences derived from four different stomach samples (R2, R3, R5, R6) were each cloned into plasmid vector pGEM-T (Promega Biotech) according to the manufacturer's instructions and transformed into *Escherichia coli* JM109 using standard procedures. Plasmids were purified using the Easy Prep Plasmid Preparation Kit (Pharmacia Biotech). Sequences were determined by the T7-sequencing system (Pharmacia

Biotech). Two primers flanking the multiple cloning sites (T7, SP6) as well as internal primers *H390f* and *H1053r* were used (Table 2). The sequence derived from the clone of the R2 sample (R2XA) was used as reference sequence. This sequence was has been asigned Genbank Accession No. AF127028. Sequence analysis was performed with the PCGene software (Intelligenetics)

[0094] PCR amplicons of three other gastric samples (R13, R27, R28) were sequenced without prior cloning (referred to below as direct sequence analysis).

DNA cloning and sequencing for "*Candidatus* Helicobacter suis"

[0095] PCR amplimers comprising the 16S rDNA-sequences from 2 different stomachs (V2B, V4A) were cloned into plasmid vector pGEM-T (Promega Biotech) according to the manufacturer's instructions and transformed into *Escherichia coli* JM109 using standard procedures. Plasmids were purified using the Easy Prep Plasmid Prep Kit (Pharmacia Biotech). Sequences were determined by the T7-sequencing system (Pharmacia Biotech). Two primers flanking the multiple cloning sites *(T7* and *SP6)* as well as internal primers *H390f* and *H1053r* were used (Table 2). Sequence analysis was performed with the PCGene software (Intelligenetics). A reference sequence was determined based on its high length and was compared to the new sequencve and the other derived sequences, to check its integrity (see Figures 4 and 5). The reference sequence V2BXA was assigned Genbank Accession No. AF127028.

[0096] PCR amplicons of three other gastric samples (V5, V14, V19) were sequenced without prior cloning (referred to below as direct sequence analysis).

Phylogenetic analysis for "*Candidatus* Helicobacter bovis"

[0097] Phylogenetic analysis was performed using the GeneCompar 2.0 software package (Applied Maths). Sequences of strains belonging to the epsilon subdivision (Table 3) were retrieved from the EMBL data library and were aligned with reference sequence R2XA. A similarity matrix was constructed from the aligned sequences and was corrected for multiple base changes by the method of Jukes & Cantor (1969). Unknown bases and gaps were not considered in the numerical analysis. A phylogenetic tree was constructed using the neighbour-joining method of Saitou & Nei (1987).

Phylogenetic analysis for "*Candidatus* Helicobacter suis"

[0098] Phylogenetic analysis was performed using the GeneCompar 2.0 software package (Applied Maths). All five "*Candidatus* Helicobacter suis" sequences and the sequences of strains belonging to the same phylogenetic lineage (Table 3) were aligned. Using the neighbour-joining method, a phylogenetic tree and corresponding similarity matrix was constructed. Unknown bases and gaps were not considered in the numerical analysis

"Candidatus Helicobacter bovis" specific PCR-assay

[0099] "*Candidatus* Helicobacter bovis" specific oligonucleotides *R574f and* R832r (Table 2), were selected from variable rDNA regions of the sequences determined by direct and indirect sequence analysis. These primers comprised a 259 bp 16S rDNA-fragment and were used to develop a specific PCR and an *in situ* hybridisation procedure. Within this fragment an internal "*Candidatus* Helicobacter bovis" specific probe R628f (Table 2) was selected for southern blot hybridisation purposes.

[0100] PCR reactions were performed in a volume of 50 µl containing 10 mM Tris HCl (pH 8.3), 50 mM KCl, 2.5 mM $MgCl_2$ 200 µM of each deoxynucleoside triphosphate, 1.5 U of AmpliTaq Gold, and 25 pmol of both forward and reverse primer. PCR amplification was performed under the following conditions: 9 min preincubation at 94 °C to activate AmpliTaq Gold, followed by 40 cycles of 30 s at 94 °C, 45 s at 60 °C and 90 s at 72 °C. Final extension was performed for 5 min at 72 °C. All gastric DNA-extracts were tested with this PCR. For positive controls, plasmid DNA was used from the cloned 16S rDNA fragments (R2XA). As a negative control a DNA-extract was used from an abomasum lacking of *Helicobacter-like* organisms.

[0101] Specificity of the "*Candidatus* Helicobacter bovis" specific oligonucleotides *R574f* and *R832r* was tested by PCR using DNA-extracts of 15 different *Helicobacter* strains and a *Wolinella succinogenes* strain (Table 1).

[0102] PCR products were separated on 2 % agarose gels, stained with ethidium bromide and transferred to Hybond N+ (Amersham) by electro-elution. Southern blot hybridisation was performed with the [γ^{32P}] ATP labelled probe *R628f* (Table 2) according to standard procedures (Amersham Pharmacia Biotech). In order to ensure the specificity of the probe hybridisation, blots were washed twice with 0.1 x SSC + 0.1 % SDS at 55°C.

"*Candidatus* Helicobacter suis" specific diagnostic PCR-assay and Southern blot hybridisation

[0103] "*Candidatus* Helicobacter suis"- specific primers (V832f and *V1261r)* were selected from variable rDNA regions of the sequences determined by direct and indirect sequence analysis, comprising a ~0.4-Kb 16S rDNA-fragment. Within this fragment a "*Candidatus* Helicobacter suis"-specific probe *V1000f* (Table 2) was selected for hybridisation purposes. PCR reactions were performed in a volume of 50 pl containing 10 mM Tris HCl (pH 8.3), 50 mM KCl, 2.5 mM $MgCl_2$, 200 µM of each deoxynucleoside triphosphate, 1.5 U of AmpliTaq Gold (Perkin-Elmer), and 25 pmol of both forward and reverse primer (Eurogentec). PCR amplification was performed under the following conditions: 9 min preincubation at 94 °C to activate AmpliTaq Gold, followed by 40 cycles of 30 s at 94 °C, 45 s at 60 °C and 90 s at 72 °C. Final extension was performed for 5 min at 72 °C. As a positive control, plasmid DNA was used from the cloned 16S rDNA fragments (V2B, V4A). As a negative control DNA extracted from the stomach of a gnotobiotic piglet was used.

[0104] To test the specificity of the primers, PCR was also performed on DNA-extracts of 15 different *Helicobacter* species. (Table 1).

[0105] PCR products were separated on 2% agarose gels, stained with ethidium bromide and transferred to Hybond N+ (Amersham) by electro-blotting. Southern blot hybridisation was performed with the [γ^{32}P] ATP-labelled probe *V1000f* according to standard procedures (Amersham Pharmacia Biotech). In order to ensure the specificity of the probe hybridisation, blots were washed twice with 0.1 x SSC + 0.1 % SDS at 55°C.

***In situ* hybridisation for "*Candidatus* Helicobacter bovis"**

[0106] In order to make the link between the "*Candidatus* Helicobacter bovis" specific probe and the bacterial spiral cells observed in the tissue sections, an *in situ* hybridisation procedure was performed on the formalin fixed and paraffin embedded pyloric samples of each animal. A 259-base digoxigenin-labeled probe was synthesized using the "PCR Dig Probe Synthesis Kit" (Boehringer Mannheim) in combination with the "*Candidatus* Helicobacter bovis" specific primers *R574f* and *R832r* (Table 2). PCR conditions were identical to those described in the diagnostic PCR assay. The resulting PCR product was purified using the "High Pure PCR Product Purification Kit" (Boehringer Mannheim) following manufacturer's instructions.

[0107] To avoid RNA'se activity, all glassware was heated at 180°C for 3 hours. Further precautions included the use of RNA'se-free water, and the use of sterile disposable materials whenever possible. Sections of the paraffin-embedded tissues (4 µm thick) were mounted on RNA'se-free, APES-coated slides (Sigma-Aldrich) and fixed by heating for 1 hour at 60 °C. The sections were deparaffinized in xylene (2x5 min), rehydrated through graded ethanol, and washed twice in PBS for 5 min each. Sections were then treated with proteinase K (DAKO) for 15 min each at 37 °C in a humidified chamber. The enzyme was inactivated by treatment with 0.2 % glycine in PBS for 3 min. Sections were washed twice in PBS for 5 min each, dehydrated in graded ethanol and air dried. Tissues were circumlined with a DAKO Pen (DAKO) to avoid liquid spillage during further processing and to ensure an efficient sealing of the coverslip. For the hybridisation step, sections were covered with 5 to 15 pl solution, containing 5 ng/µl labeled probe in 50 % deionized formamide, 2x SCC, 10 % dextran sulfate, 0.25 µg/µl yeast t-RNA, 0.5 µg/µl heat denatured salmon sperm DNA, and lx Denhart's solution. Sections were covered with a piece of coverslip to avoid evaporation. To denature the probe, sections were heated for 10 min at 95 °C and chilled on ice for 10 min. Slides were then hybridised overnight at 37 °C in a humidified chamber. To remove the unbound probe, the coverslips were removed and the sections were washed in 2x SCC and 1x SCC at room temperature for 10 min each followed by two washes of 0.3x SCC at 40 °C for 10 min and at room temperature for 10 min, respectively.

[0108] All steps involving the immunological detection of the hybridised probe were performed at room temperature. The sections were treated first for 30 minutes in Buffer 1 (100mM Tris HCl, 150 mM NaCl, pH 7.5) containing 2 % normal goat serum and 0.3 % Triton X-100. An incubation step followed for 3 hours with diluted (1:30 in the same solution) anti-digoxigenin antibodies conjugated to horse-radish peroxidase (DAKO). Unbound antibodies were washed gently on a shaker with Buffer 1 followed by Buffer 2 (100 mM Tris HCl, 100 mM NaCl, 50 mM $MgCl_2$, pH 9.5) for 15 min each. To optimize the detection level, the "Tyramid Signal Amplification System" (NEN Life Science Products) was applied on each section, following manufacturer's instructions. The hybridised probe was then visualized, using H_2O_2 with diaminobenzidine as a chromogen (Fast DAB Tablet Set, Sigma-Aldrich). Thereafter the sections were counter-stained with Mayer's hematoxylin and mounted.

***In situ* hybridisation for "*Candidatus* Helicobacter suis"**

[0109] To link the derived sequence to the corresponding organism, an *in situ* hybridisation procedure was performed on the formalin fixed and paraffin embedded pyloric samples of each animal. A ~0.4 Kb digoxigenin-labeled probe was synthesized using the "PCR Dig Probe Synthesis Kit" (Boehringer Mannheim) in combination with the "Candidatus

Helicobacter suis"-specific primers *V832f* and *V1261r* (Table 2). The rest of the method was performed as mentioned above for "Candidatus Helicobacter bovis".

Nucleotide sequence accession numbers

[0110] Accession numbers of the 16S rDNA gene sequences used for the phylogenetic analysis are listed in table 3.

[0111] The 16S rDNA nucleotide sequence of "*Candidatus* Helicobacter bovis" has been deposited in the Genbank database under accession number AF127027.

[0112] The 16S rDNA nucleotide sequence of "*Candidatus* Helicobacter suis" has been deposited in the Genbank database under accession number AF127028.

Results

Urease activity and immunohistochemical evaluation for the cattle samples

[0113] Urease activity was observed in all pyloric samples (7/7). In the fundic samples, urease activity was absent (0/7). Spiral immunostained organisms were observed in the pyloric samples of all animals. The highest concentration was seen in the most distal pyloric samples. They were mostly situated in the mucus layer and in the lumen of the proximal part of the gastric crypts where they formed small clusters. In some samples, coccoid organisms, were observed between the spiral bacteria, which also crossreacted with the *H. pylori* polyclonal antibodies. In the positive control only *Helicobacter pylori* - like bacteria were stained while in the negative controls no staining was observed.

Urease activity and immunohistochemical evaluation for the pig samples

[0114] Tightly coiled immunostained spiral organisms, morphologically similar to "*Gastrospirillum suis*" (Queiroz et al., 1990) were observed in all stomachs (5/5), which was consistent with the presence of urease activity (5/5). The gastrospirillum-like organisms were seen laying separately or in small clusters with a patchy distribution over the sample, and were found mostly in the superficial part of the gastric crypts. Some bacteria revealed bipolar immunostained flagellae. Immunostained coccoid-like organisms were also observed in the pyloric crypts. In the positive control, only *Helicobacter pylori-like* bacteria were stained while in the negative controls no labeling was observed.

Transmission electronmicroscopy for "*Candidatus* Helicobacter bovis"

[0115] Large groups of multiple spiral bacteria were seen within the crypts of the gastric mucosa. There was no obvious cell association between the bacteria and the gastric cells, neither were there any intracellular bacterial inclusions. The bacteria were helical-shaped and had 1-3 complete spiral turns per cell with a wavelength of approximately 750 nm. Cells were 1 - 2.5 µm long and 0.3 µm wide. At least four flagelles were seen at one end. It was unclear whether these flagellae were uni- or bipolar, neither could the presence or absence of a flagella sheath be noted.

Transmission electronmicroscopy for "*Candidatus* Helicobacter suis"

[0116] Within the gastric crypts of the antral region, longitudinal and transversal sections of spiral organisms could be seen. All bacteria had the same characteristic tightly coiled appearance, typical of *Helicobacters* with the gastrospirillum morphology. The length of cells varied from 2.5 to 3.5 pm and they were approximately 0.6 pm wide. Multiple complete spiral turns with a wavelength of ± 600 nm were seen in all longitudinal sections. As only few longitudinal sections of the bacteria were obtained, the number and implantation of the flagellae could not be studied although partial fragments were observed. The bacteria were not seen intracellularly nor was there any obvious cell association with the surrounding epithelial cells. The presence or absence of a flagella sheath could not be noted.

Amplification, cloning and sequencing of *Helicobacter-like* 16S rDNA fragments from cattle samples

[0117] PCR amplification of the 16S rRNA gene using the *H33f and H1368r* primers, produced a fragment of the expected size range (± 1.3 Kbp) in all seven samples examined. Partial direct sequence analysis of four of these bands (R2, R3, R5, R6) and subsequent database comparison (BLAST) confirmed the PCR products to be *Helicobacter*-like 16S rDNA fragments. Four PCR products (R2, R3, R5, R6) were cloned followed by partial screening. In one clone a *Clostridium*-like 16S rDNA fragment was found. In all other clones *Helicobacter*-like fragments were inserted. The 16S rDNA sequences of four clones derived from different animals (R2XA, R3XA, R5XE, R6XA), were determined. Additional sequences of three other samples (R13, R27, R28) were characterized by direct sequence analysis using the

primers *H33f, H1368r, H390f* and *H1053r.*

Amplification, cloning and sequencing of *Helicobacter*-like 16S rDNA fragments from pig samples

[0118] Several combinations of PCR primers yielded sequences of the expected size. The length of these amplified fragments varied between 1.2 Kb *(H274f-1492RPL)* and 1.4 Kb *(H61f-1492RPL).* The latter primer combination was used to examine all samples. The 16S rDNA sequences of two different clones were determined (V2BXA, V4AXA). Additional sequences of 3 other samples (V5, V14, V19) were determined by direct sequence analysis.

Sequences and phylogenetic analysis for cattle samples

[0119] Sequence length varied from 1267 to 1335 basepairs. Pairwise comparisons between these 7 sequences revealed a sequence homology of more than 99 %. One reference sequence (R2XA) of 1335 bp (see Figure 1: SEQ ID NO 1) was selected for phylogenetic evaluation. A similarity matrix based on comparisons of 16S rRNA sequences of 23 strains representing all validly named *Helicobacter* species, **Helicobacter heilmannii*** (type1, type2), *Campylobacter jejuni, Arcobacter cryaerophilus* and *Wollinella succinogenes* was calculated. By this analysis it was shown that the sequences of the bovine *Helicobacter*-like organisms form a distinct group within the genus *Helicobacter* with *Helicobacter bilis* as closest taxonomic relative (level of similarity 92.8 %). The reference sequence was clearly distinct from sequences belonging to other superfamily VI genera, as shown by a 85.6, 85.1 % and 89.7 % homology with *Campylobacter jejuni, Arcobacter butzleri* and *Wolinella succinogenes* respectively. A phylogenetic tree based on this analysis is shown in Fig. 3A.

Sequences and phylogenetic analysis for pig samples

[0120] The 5 sequences that were determined had lengths varying from 1345 to 1421 basepairs. Pairwise comparisons between 1345 bp consensus fragments of these sequences, revealed a minimum homology of 97.7 %. One reference sequence of 1421 bp, obtained from PCR product 2BXA (see Figure 2: SEQ ID NO 2), was used for phylogenetic analysis. A similarity matrix was calculated based on comparisons of 16S rDNA sequences of all *Helicobacter* species, **Helicobacter heilmannii*** type 1 and type 2, *Campylobacter jejuni, Arcobacter butzleri* and *Wollinella succinogenes* (Table 3). In this analysis, the sequence of the porcine gastrospirillum-like organism formed a distinct subgroup within the *Helicobacter* lineage together with other gastrospirilla: *Helicobacter felis,* H. *bizzozeronii, H. salomonis,* **H. heilmannii*** type 1 and type 2. The sequence was highly similar to that of **H. heilmannii*** type 1 (level of similarity 99.5 %). The similarity level of other gastrospirillum-like bacteria, H. *felis, H. bizzozeronii,* H. *salomonis* and H. *heilmanni* type 2 was 96.4 %, 95.5 %, 96.6 % and 96.8 % respectively. The reference sequence was clearly distinct from sequences belonging to other superfamily VI-genera, as shown by a 86.2 %, 84.7 % and 89.6 % homology with *Campylobacter jejuni, Arcobacter butzleri* and *Wolinella succinogenes* respectively.

[0121] A phylogenetic tree based on this analysis is shown in Figure 3B.

***Diagnostic PCR-assay for "Candidatus* Helicobacter bovis"**

[0122] A 259 base fragment was produced for all seven stomach samples with primer pair *R574f-R832r.* All PCR products crosshybridised with the *R628f* probe after southern blot hybridisation. No amplification product was obtained using DNA preparations from any of the *Helicobacter* strains, nor from the bovine *Wolinella succinogens* strain (Table 1). The positive control yielded a ~0.3 Kb product as expected. There was no DNA-amplification using the negative control material.

"*Candidatus* Helicobacter suis"-specific PCR and Southern blot hybridisation

[0123] Amplification of *Helicobacter* DNA using the primers *V832f* and *V1261r* produced a 433-base fragment from all five stomach samples. All PCR products hybridised with the *V1000f* probe after Southern blot hybridisation. No amplification product was obtained using DNA preparations from any of the *Helicobacter* strains including *H. felis, H. bizzozeronii* and *H. salomonis* (Table 1), nor from the negative control. PCR with the cloned reference material (2BXA) yielded a ~0.4 Kb product as expected.

***In situ* hybridisation for "*Candidatus* Helicobacter bovis"**

[0124] *In situ* hybridisation of the bovine *Helicobacter-like* bacteria with the *"Candidatus* Helicobacter bovis"- specific probe was seen in sections from all (7/7) stomachs. These bacteria were observed as darkbrown spiral organisms,

organised in small clusters, situated in the gastric crypts of the pyloric part of the abomasal stomach. Not all spiral bacteria were stained. Sometimes a faint background, seen as fine stained strings, was observed in the surrounding cells. This background staining was also observed in the *H. pylori*-infected mouse stomach which was used as a negative control. The *H. pylori* cells in this control though did not hybridise with the "*Candidatus Helicobacter bovis*"-specific probe.

***In situ* hybridisation for "*Candidatus* Helicobacter suis"**

[0125] *In situ* hybridisation of "*Gastrospirillum suis*"-like bacteria with the "*Candidatus* Helicobacter suis"- specific probe was seen in sections from all (5/5) stomachs. Bacteria were observed as darkbrown spiral organisms in the superficial mucus layer and the gastric crypts. In some cases, helical organisms located deeply in the crypts, were weakly labeled or were negative. Sometimes a faint background, seen as fine stained strings, was observed in the surrounding cells. This background staining was also observed in the *H.* pylori-infected mouse stomach which was used as a negative control. The *H. pylori* cells in this control though did not hybridise with the "*Candidatus* Helicobacter suis"- specific probe.

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Table 1:

Bacterial strains used for the evaluation of the *"Candidatus* Helicobacter bovis" specific PCR

Taxon	Source	Collection N° or Strain
Helicobacter acinonychis	Cheetah gastric mucosa	LMG 12684^T
Helicobacter cinaedi	Human feces	LMG 7543 ^{T}
Helicobacter sp. strain CLO-3	Human rectal swab	LMG 7792
Helicobacter fennelliae	Human feces	LMG 11759
Helicobacter pametensis	Tern feces	LMG 12678 ^{T}
Helicobacter sp. strain Bird B	Bird feces	LMG 12679
Helicobacter sp. strain Bird C	Bird feces	LMG 13642
Helicobacter hepaticus	Murine liver	LMG 16316^T
Helicobacter pullorum	Chicken lower bowel	LMG 16318
Helicobacter mustelae	Ferret gastric mucosa	LMG 18044 ^{T}
Helicobacter canis	Canine feces	LMG 18086 ^{T}
Helicobacter muridarum	Murine intestinal mucosa	LMG 14378 ^{T}
Helicobacter bizzozeronii	Canine gastric mucosa	Strain 12A
Helicobacter salonionis	Canine gastric mucosa	CCUG 37845 T
Helicobacter felis	Feline gastric mucosa	CCUG 28539 T

Table 2: Oligonucleotide primers and probe used for PCR amplification, sequencing of genes coding for 16S rRNA and Southern blot hybridisation

Primers	Sequences (5'-3')	*Escherichia coli* 16S rRNA position
H33f	ACG CTG GCG GCG TGC CTA ATA CAT GCA AGT CG	33-64 (SEQ ID NO 3)
H1368r	GGT GAG TAC AAG ACC CGG GAA CGT ATT CAC CG	1368-1388 (SEQ ID NO 4)
H390f	GCA GCA ACG CCG CGT GGA GGA TGA	390-413 (SEQ ID NO 5)
H1053r	ACG AGC TGA CGA CAG CCG TG	1053-1072 (SEQ ID NO 6)
R574f	AGA GCG TGT AGG CGG AAT GAT	574-593 (SEQ ID NO 7)
R628f	AAC TGC GTT TGA AAC TAT CAT T	628-649 (SEQ ID NO 8)
H61f	TGC AAG TCG AAC GAT GAA GC	61-76 (SEQ ID NO 9)
H274f	AGG CTA TGA CGG GTA TCC GGC CTG AGA	274-299 (SEQ ID NO 10)
1492RPL	GCC GCC CGG GTT ACC TTG TTA CGA CTT	832-852 (SEQ ID NO 11)
V832f	TTG GGA GGC TTT GTC TTT CCA	1000-1020 (SEQ ID NO 12)
V1261r	GAT TAG CTC TGC CTC GCG GCT	1261-1281 (SEQ ID NO 13)

V1000f	AGG AAT TCC CTA GAA ATA GGG	1000-1020 (SEQ ID NO 26)
R832r	CGA GGA GAC AAG CCC CCC GA	832-851 (SEQ ID NO 14)

Table 3:

Sources and accession numbers of strains used for phylogenetic analysis.

Taxon	Source	Genbank Accession N°
*"Gastrospirillum hominis" type 1	Human gastric mucosa	L10079
*"Gastrospirillum hominis" type 2	Human gastric mucosa	L10080
Helicobacter acinonychis	Cheetahgastric mucosa	M88148
Helicobacter bilis	Murine liver	U18766
Helicobacter bizzozeronii	Canine gastric mucosa	Y09404
Helicobacter canis	Canine feces	L13464
Helicobacter cholecystus	Murine liver	U46129
Helicobacter cinaedi	Human feces	M88150
Helicobacter felis	Feline gastric mucosa	M57398
Helicobacter fennelliae	Human feces	M88154
Helicobacter hepaticus	Murine liver	U07574
Helicobacter muridarum	Murine intestinal mucosa	M80205
Helicobacter mustelae	Ferret gastric mucosa	M35048
Helicobacter nemestrinae	Macaque gastric mucosa	X67854
Helicobacter pametensis	Swine feces	M88155
Helicobacter pullorum	Broiler chicken cecum	L36141
Helicobacter pylori	Human gastric mucosa	M88157
Helicobacter salomonis	Canine gastric mucosa	Y09405
Helicobacter trogontum	Rat colon mucosa	U65103
Helicobacter rodentium	Murine intestinal mucosa	U96297
Arcobacter butzleri	Human	L14626
Campylobacter jejuni	Human feces	L14630
Wolinella succinogenes	Cattle abomasal mucosa	M88159

Annex to the application documents - subsquently filed sequences listing

[0185]

SEQUENCE LISTING

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<120> New gastric Helicobacter 16 S rDNA sequences from cattle and pigs and their use for detection and typing of Helicobacter strains

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Claims

1. An isolated 16S rDNA *Helicobacter* polynucleic acid sequence selected from any of the following

   (a) a sequence represented in any of SEQ ID NO 1 to 2, or, the 16S rRNA sequence encoded thereby,

   (b) a sequence which hybridizes under stringent conditions to any of the sequences defined in (a).

2. An isolated polynucleid acid sequence according to claim 1 represented by any of SEQ ID NO 1 to 2 or 15 to 24.

3. An isolated polynucleic acid sequence according to claim 1 which is more than 92.8%, preferably more than 93.5%, more preferably more than 95% and most preferably more than 97.5% homologous to SEQ ID NO 1.

4. A part of an isolated polynucleic acid according to any of claims 1 to 3, wherein said part is unique to the polynucleic acid sequence it is derived from.

5. A probe which specifically hybridizes to a polynucleic acid sequence according to any of claims 1 to 4.

6. A primer which specifically amplifies a polynucleic acid sequence according to any of claims 1 to 4.

7. A method for detection and/or typing of *Helicobacter* strains present in a biological sample comprising hybridizing the 16S rRNA gene target region polynucleotides of said *Helicobacter* strains present in said biological sample with at least one probe according to claim 5.

8. A method for detection and/or typing of *Helicobacter* strains present in a biological sample comprising specifically amplifying the 16S rRNA gene target region polynucleotides of said *Helicobacter* strains present in said biological sample with at least one primer according to claim 6.

9. A method for detection and/or typing of *Helicobacter* strains present in a biological sample comprising specifically hybridizing or specifically amplifying the 16S rRNA gene target region polynucleotides of said *Helicobacter* strains present in said biological sample with at least one sequence which is more than 96.6% homologous to SEQ ID NO 2, or a sequence specific primer or a sequence specific probe derived thereof.

10. A diagnostic kit for detection and/or typing of *Helicobacter* strains comprising:

- at least one probe according to claim 5 or 9, and/or,
- at least one primer according to claim 6 or 9.

11. A medicament comprising a polynucleic acid sequence according to any of claims 1 to 6.

12. A polynucleic acid sequence according to any of claims 1 to 6 for use as a medicament.

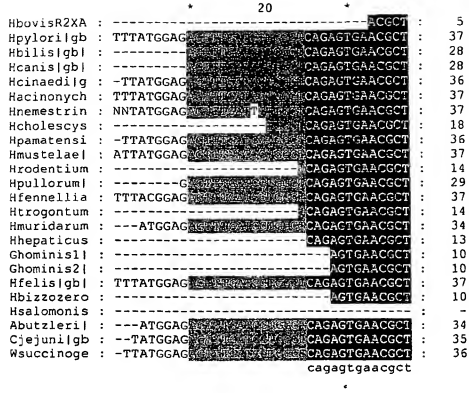

* 20 *
HbovisR2XA : ----------CGCT : 5
Hpylori|gb : TTTATGGAGCAGAGTGAACGCT : 37
Hbilis|gb| : ---------CAGAGTGAACGCT : 28
Hcanis|gb| : ---------CAGAGTGAACGCT : 28
Hcinaedi|g : -TTATGGAGCAGAGTGAACGCT : 36
Hacinonych : TTTATGGAGCAGAGTGAACGCT : 37
Hnemestrin : NNTATGGAGCAGAGTGAACGCT : 37
Hcholescys : ----------CAGAGTGAACGCT : 18
Hpamatensi : -TTATGGAGCAGAGTGAACGCT : 36
Hmustelae| : ATTATGGAGCAGAGTGAACGCT : 37
Hrodentium : ----------CAGAGTGAACGCT : 14
Hpullorum| : --------GCAGAGTGAACGCT : 29
Hfennellia : TTTACGGAGCAGAGTGAACGCT : 37
Htrogontum : ----------CAGAGTGAACGCT : 14
Hmuridarum : ---ATGGAGCAGAGTGAACGCT : 34
Hhepaticus : ----------CAGAGTGAACGCT : 13
Ghominis1| : ----------AGTGAACGCT : 10
Ghominis2| : ----------AGTGAACGCT : 10
Hfelis|gb| : TTTATGGAGCAGAGTGAACGCT : 37
Hbizzozero : ----------AGTGAACGCT : 10
Hsalomonis : ---------- : -
Abutzleri| : ---ATGGAGCAGAGTGAACGCT : 34
Cjejuni|gb : --TATGGAGCAGAGTGAACGCT : 35
Wsuccinoge : -TTATGGAGCAGAGTGAACGCT : 36
cagagtgaacgct
*

Figure 1 - 1

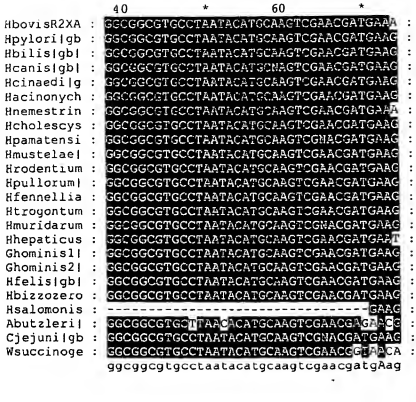

40 * 60 *
HbovisR2XA : GCCGGCGTGCCTAATACATGCAACTCGAACGATGAAA : 42
Hpylori|gb : GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG : 74
Hbilis|gb| : GGCGGGGTGCCTAATACATGCAAGTCGAACGATGAAG : 65
Hcanis|gb| : GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG : 65
Hcinaedi|g : GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG : 73
Hacinonych : GGCGGGCGTGCCTAATACATGCAAGTCGAACGATGAAG : 74
Hnemestrin : GGCGGGCGTGCCTAATACATGCAAGTCGAACGATGAAA : 74
Hcholescys : GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG : 55
Hpamatensi : GGCGGCGTGCCTAATACATGCAAGTCGNACGATGAAG : 73
Hmustelae| : GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG : 74
Hrodentium : GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG : 51
Hpullorum| : GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG : 66
Hfennellia : GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG : 74
Htrogontum : GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG : 51
Hmuridarum : GGCGGCGTGCCTAATACATGCAAGTCGNACGATGAAG : 71
Hhepaticus : GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAT : 50
Ghominis1| : GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG : 47
Ghominis2| : GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG : 47
Hfelis|gb| : GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG : 74
Hbizzozero : GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG : 47
Hsalomonis : ----------GAAG : 4
Abutzleri| : GGCGGCGTGCTTAACACATGCAAGTCGAACGAGAACG : 71
Cjejuni|gb : GGCGGCGTGCCTAATACATGCAAGTCGNACGATGAAG : 72
Wsuccinoge : GGCGGCGTGCCTAATACATGCAAGTCGAACGCGAACA : 73
ggcggcgtgcctaatacatgcaagtcgaacgatgAag

Figure 1 - 2

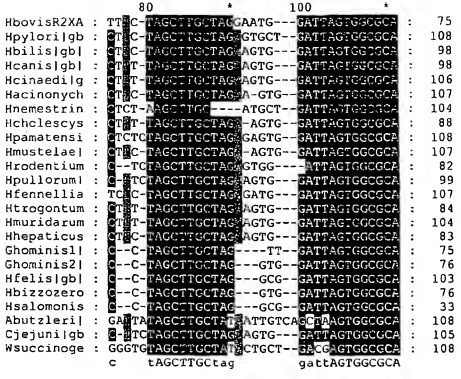

80
*
100
*
HbovisR2XA : TTGC-TAGCTTGCTAGCAATG---GATTAGTGGCGCA : 75
Hpylori|gb : CTGC-TAGCTTGCTAGCGTGCT--GATTAGTGGCGCA : 108
Hbilis|gb| : CTGC-TAGCTTGCTAGCAGTG---GATTAGTGGCGCA : 98
Hcanis|gb| : CTGT-TAGCTTGCTAGCAGTG---GATTAGTGGCGCA : 98
Hcinaedi|g : CTGT-TAGCTTGCTAGCAGTG---GATTAGTGGCGCA : 106
Hacinonych : CTGC-TAGCTTGCTAGCA-GTG--GATTAGTGGCGCA : 107
Hnemestrin : CTCT-AAGCTTGC----ATGCT--GATTAGTGGCGCA : 104
Hchclescys : CTGT-TAGCTTGCTAGCA-AGTG--GATTAGTGGCGCA : 88
Hpamatensi : CTCTCTAGCTTGCTAGCGAGTG--GATTAGTGGCGCA : 108
Hmustelae| : CTGC-TAGCTTGCTAGCA-AGTG--GATTAGTGGCGCA : 107
Hrodentium : C--TCTAGCTTGCTAGCGTGG----ATTAGTGGCGCA : 82
Hpullorum| : C-GTCTAGCTTGCTAGCAGTG---GATTAGTGGCGCA : 99
Hfennellia : TCGC-TAGCTTGCTAGCGATG---GATTAGTGGCGCA : 107
Htrogontum : CTGT-TAGCTTGCTAGCAGTG---GATTAGTGGCGCA : 84
Hmuridarum : CTGT-TAGCTTGCTAGCAGTG---GATTAGTGGCGCA : 104
Hhepaticus : CTGC-TAGCTTGCTAGCAGTG---GATTAGTGGCGCA : 83
Ghominis1| : C--C-TAGCTTGCTAG----TT--GATTAGTGGCGCA : 75
Ghominis2| : C--C-TAGCTTGCTAG---GTG--GATTAGTGGCGCA : 76
Hfelis|gb| : C--C-TAGCTTGCTAG---GCG--GATTAGTGGCGCA : 103
Hbizzozero : C--C-TAGCTTGCTAG---GTG--GATTAGTGGCGCA : 76
Hsalomonis : C--C-TAGCTTGCTAG---GCG--GATTAGTGGCGCA : 33
Abutzleri| : GATTATAGCTTGCTATTATTGTCAGCATAGTGGCGCA : 108
Cjejuni|gb : CGTCTAGCTTGCTAGCAGTG---GATTAGTGGCGCA : 105
Wsuccinoge : GGGTGTAGCTTGCTATGCTGCT--GACGAGTGGCGCA : 108
c tAGCTTGCtag gattAGTGGCGCA

Figure 1 _ 3

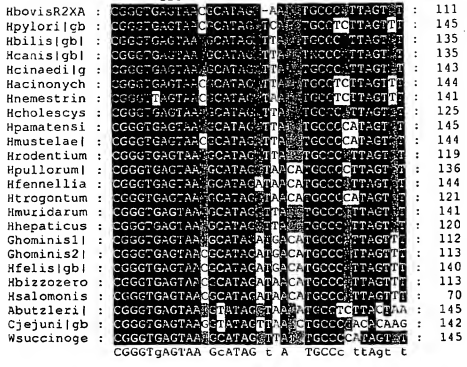

120 * 140
HbovisR2XA : 111
Hpylori|gb : 145
Hbilis|gb| : 135
Hcanis|gb| : 135
Hcinaedi|g : 143
Hacinonych : 144
Hnemestrin : 141
Hcholescys : 125
Hpamatensi : 145
Hmustelae| : 144
Hrodentium : 119
Hpullorum| : 136
Hfennellia : 144
Htrogontum : 121
Hmuridarum : 141
Hhepaticus : 120
Ghominis1| : 112
Ghominis2| : 113
Hfelis|gb| : 140
Hbizzozero : 113
Hsalomonis : 70
Abutzleri| : 145
Cjejuni|gb : 142
Wsuccinoge : 145
CGGGTgAGTAA GcATAG t A TGCCc ttAgt t

Figure 1 - 4


* 160 * 180
HbovisR2XA : GGGATAGCCA G GGAAAC GTGATTAATAC TA ATAC : 148
Hpylori|gb : GGGATAGCCA T GGAAACGA TGATTAATAC CA ATAC : 182
Hbilis|gb| : GGGATAGCCA TGGAAACGGTGATTAATAC TG ATAC : 172
Hcanis|gb| : GGGATAGCCA TGGAAACGGTGATTAATAC TG ATAC : 172
Hcinaedi|g : GGGATAGCCA TGGAAACGGTGATTAATAC TG ATAC : 180
Hacinonych : GGGATAGCCA TGGAAACGGTGATTAATAC CA ATAT : 181
Hnemestrin : GGGATAGCCA TGGAAACGA AGA TAATAC CA ATAC : 178
Hcholescys : GGGATAGCCA TGGAAACGGTGATTAATAC CG ATAC : 162
Hpamatensi : GGGATAGCCA TGGAAACGGTGATTAATAC TA ATAC : 182
Hmustelae| : GGGATAGCCA TGGAAACGGTGATTAATAC TG ATAC : 181
Hrodentium : AGGATAGCCA TGGAAACGA TGATTAATAC TG ATAC : 156
Hpullorum| : GGGATAGCCA TGGAAACGGTGATTAATAC TA ATAC : 173
Hfennellia : AGGATANNNN NNGAAACGGTGATTAATAC NN NNNN : 181
Htrogontum : GGGATAGCCA TGGAAACGGCCATTAATAC CG ATAC : 158
Hmuridarum : GGGATAGCCA TGGAAACGGTGATTAATAC TG ATAC : 178
Hhepaticus : GGGATAGCCA TGGAAACGGTGATTAATAC TG ATAC : 157
Ghominis1| : GGATAGCCA TA GAAA TGGTGATTAATAC CAA ATAC : 149
Ghominis2| : GGGATAGCCA TA GAAA TGGTGATTAATAC CAA ATAT : 150
Hfelis|gb| : GGGATAGCCA TA GAAA TGGTGATTAATAC CAA ATAC : 177
Hbizzozero : GGGATAGCCA TA GAAA TGGTGATTAATAC CAA ATAC : 150
Hsalomonis : GGGATAGCCA TA GAAA TGGTGATTAATAC CAA ATAC : 107
Abutzleri| : GGGATA AC AA TTGGAAACGA TTGC AAA AC CTT ATA T : 182
Cjejuni|gb : AGGAC AC AGT TGGAAACGACTGC AA AC TCT ATAC : 179
Wsuccinoge : GGATAGCCA TGGAAACGGTGATTAATAC GG ATAT : 182
gGgAtAgCca tgGAAAcggtgatTAATAC ATAc

Figure 1 -5

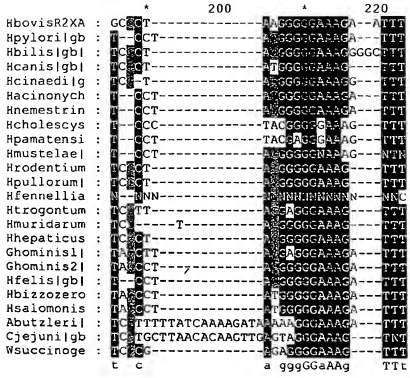

200
220
HbovisR2XA : GCGCT---------- AAGGGGGAAAGA--ATTT : 169
Hpylori|gb : A--CCT---------- AAGGGGGAAAGA---TTT : 201
Hbilis|gb| : ACGCT---------- AAGGGGAAAGGGGCTTT : 195
Hcanis|gb| : ACGCT---------- ATGGGGAAAG----TTT : 191
Hcinaedi|g : ACG-T---------- AAGGGGAAAG----TTT : 199
Hacinonych : A--CCT---------- AAGGGGAAAGA---TTT : 200
Hnemestrin : A--CCT---------- AAGGGCAAAGA---TTT : 197
Hcholescys : A--CCC---------- TACGGGGGAAAG---TTT : 181
Hpamatensi : A--CCT---------- TACGAGGGAAAG---TTT : 201
Hmustelae| : A--CCT---------- AGGGGGCAAAG---NTN : 200
Hrodentium : ACGCT---------- AAGGGGGAAAG----TTT : 175
Hpullorum| : ACGCT---------- AAGGGGGAAAG----TTT : 192
Hfennellia : A--NNN---------- ANNNHNNNNN---NNC : 200
Htrogontum : ACGTT---------- AAGAGGGAAAG----TTT : 177
Hmuridarum : ACG------T---------- AAGGGGGAAAG----TTT : 196
Hhepaticus : ACGCT---------- AAGGGGGAAAG----TTT : 176
Ghominis1| : AAGCTT---------- AAGAGGGAAAGA---TTT : 170
Ghominis2| : AAGCCT---7---------- AAGGGGGAAAGA---TTT : 171
Hfelis|gb| : A--CCT---------- AAGGGGGAAAGA---TTT : 196
Hbizzozero : AAGCCT---------- ATGGGGGAAAGA---TTT : 171
Hsalomonis : AAGCCT---------- ATGGGGGAAAGA---TTT : 128
Abutzleri| : ACGTTTTTATCAAAAGATAAAAGGGAAAGA---TTT : 216
Cjejuni|gb : ACTGCTTAACACAAGTTGAGTAGGGAAAG----TNT : 212
Wsuccinoge : ACGCG---------- AGAGGGGAAAG----TTT : 201
t c a gggGGaAAg TTt

Figure 1 - 6

```
                    *       240         *       26
HbovisR2XA  : ------------------------------------ :    -
Hpylori|gb  : ------------------------------------ :    -
Hbilis|gb|  : CAATAAAGAATTTCTCTTTTTAGTGCTTTGTGTTGTT :  232
Hcanis|gb|  : ------------------------------------ :    -
Hcinaedi|g  : ------------------------------------ :    -
Hacinonych  : ------------------------------------ :    -
Hnemestrin  : ------------------------------------ :    -
Hcholescys  : ------------------------------------ :    -
Hpamatensi  : ------------------------------------ :    -
Hmustelae|  : ------------------------------------ :    -
Hrodentium  : ------------------------------------ :    -
Hpullorum|  : ------------------------------------ :    -
Hfennellia  : ------------------------------------ :    -
Htrogontum  : ------------------------------------ :    -
Hmuridarum  : ------------------------------------ :    -
Hhepaticus  : ------------------------------------ :    -
Ghominis1|  : ------------------------------------ :    -
Ghominis2|  : ------------------------------------ :    -
Hfelis|gb|  : ------------------------------------ :    -
Hbizzozero  : ------------------------------------ :    -
Hsalomonis  : ------------------------------------ :    -
Abutzleri|  : ------------------------------------ :    -
Cjejuni|gb  : ------------------------------------ :    -
Wsuccinoge  : ------------------------------------ :    -
```

Figure 1 - 7

```
                0          *        280          *
HbovisR2XA      : ------------------------------------ :     -
Hpylori|gb      : ------------------------------------ :     -
Hbilis|gb|      : GGCACAAAATTCTAGTATTTGGAATGAGAAATTGATG :   269
Hcanis|gb|      : ------------------------------------ :     -
Hcinaedi|g      : ------------------------------------ :     -
Hacinonych      : ------------------------------------ :     -
Hnemestrin      : ------------------------------------ :     -
Hcholescys      : ------------------------------------ :     -
Hpamatensi      : ------------------------------------ :     -
Hmustelae|      : ------------------------------------ :     -
Hrodentium      : ------------------------------------ :     -
Hpullorum|      : ------------------------------------ :     -
Hfennellia      : ------------------------------------ :     -
Htrogontum      : ------------------------------------ :     -
Hmuridarum      : ------------------------------------ :     -
Hhepaticus      : ------------------------------------ :     -
Ghominis1|      : ------------------------------------ :     -
Ghominis2|      : ------------------------------------ :     -
Hfelis|gb|      : ------------------------------------ :     -
Hbizzozero      : ------------------------------------ :     -
Hsalomonis      : ------------------------------------ :     -
Abutzleri|      : ------------------------------------ :     -
Cjejuni|gb      : ------------------------------------ :     -
Wsuccinoge      : ------------------------------------ :     -
```

Figure 1 - 8

```
                 300         *        320         *
HbovisR2XA  : ------------------------------------ :   -
Hpylori|gb  : ------------------------------------ :   -
Hbilis|gb|  : TTGTGAAGCAATTTGTGCGGAGACTAGACTTAGTGTC :  306
Hcanis|gb|  : ------------------------------------ :   -
Hcinaedi|g  : ------------------------------------ :   -
Hacinonych  : ------------------------------------ :   -
Hnemestrin  : ------------------------------------ :   -
Hcholescys  : ------------------------------------ :   -
Hpamatensi  : ------------------------------------ :   -
Hmustelae|  : ------------------------------------ :   -
Hrodentium  : ------------------------------------ :   -
Hpullorum|  : ------------------------------------ :   -
Hfennellia  : ------------------------------------ :   -
Htrogontum  : ------------------------------------ :   -
Hmuridarum  : ------------------------------------ :   -
Hhepaticus  : ------------------------------------ :   -
Ghominis1|  : ------------------------------------ :   -
Ghominis2|  : ------------------------------------ :   -
Hfelis|gb|  : ------------------------------------ :   -
Hbizzozero  : ------------------------------------ :   -
Hsalomonis  : ------------------------------------ :   -
Abutzleri|  : ------------------------------------ :   -
Cjejuni|gb  : ------------------------------------ :   -
Wsuccinoge  : ------------------------------------ :   -
```

Figure 1 - 9

```
                  340          *          360          *
HbovisR2XA : ------------------------------------ :     -
Hpylori|gb : ------------------------------------ :     -
Hbilis|gb| : TGTCGCACAAGCAAATTGCGAACTCATCGATTTATCG :   343
Hcanis|gb| : ------------------------------------ :     -
Hcinaedi|g : ------------------------------------ :     -
Hacinonych : ------------------------------------ :     -
Hnemestrin : ------------------------------------ :     -
Hcholescys : ------------------------------------ :     -
Hpamatensi : ------------------------------------ :     -
Hmustelae| : ------------------------------------ :     -
Hrodentium : ------------------------------------ :     -
Hpullorum| : ------------------------------------ :     -
Hfennellia : ------------------------------------ :     -
Htrogontum : ------------------------------------ :     -
Hmuridarum : ------------------------------------ :     -
Hhepaticus : ------------------------------------ :     -
Ghominis1| : ------------------------------------ :     -
Ghominis2| : ------------------------------------ :     -
Hfelis|gb| : ------------------------------------ :     -
Hbizzozero : ------------------------------------ :     -
Hsalomonis : ------------------------------------ :     -
Abutzleri| : ------------------------------------ :     -
Cjejuni|gb : ------------------------------------ :     -
Wsuccinoge : ------------------------------------ :     -
```

Figure 1 - 10

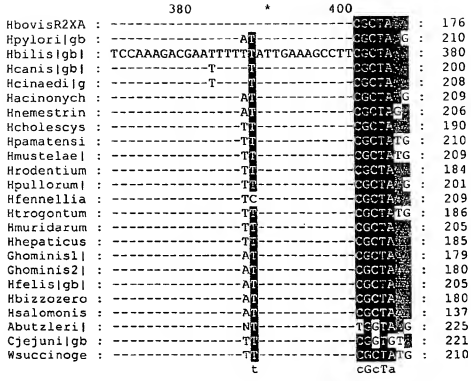

380
*
400
HbovisR2XA : ---------- : 176
Hpylori|gb : ----------A----------GGCTA--G : 210
Hbilis|gb| : TCCAAAGACGAATTTTTTATTGAAAGCCTTGGCTA-- : 380
Hcanis|gb| : ----------T----T----------GGCTA-- : 200
Hcinaedi|g : ----------T----T----------GGCTA-- : 208
Hacinonych : ----------A----T----------GGCTA--G : 209
Hnemestrin : ----------A----T----------GGCTA--G : 206
Hcholecys : ----------T----T----------GGCTA-- : 190
Hpamatensi : ----------T----T----------GGCTATG : 210
Hmustelae| : ----------T----T----------GGCTATG : 209
Hrodentium : ----------T----T----------GGCTA-- : 184
Hpullorum| : ----------T----T----------GGCTA--G : 201
Hfennellia : ----------TC---T----------GGCTA-- : 209
Htrogontum : ----------T----T----------GGCTATG : 186
Hmuridarum : ----------T----T----------GGCTA-- : 205
Hhepaticus : ----------T----T----------GGCTA-- : 185
Ghominis1| : ----------A----T----------GGCTA-- : 179
Ghominis2| : ----------A----T----------GGCTA-- : 180
Hfelis|gb| : ----------A----T----------GGCTA-- : 205
Hbizzozero : ----------A----T----------GGCTA-- : 180
Hsalomonis : ----------A----T----------GGCTA-- : 137
Abutzleri| : ----------N----T----------TGGTAAG : 225
Cjejuni|gb : ----------T----T----------GGGTGTT : 221
Wsuccinoge : ----------T----T----------GGCTATG : 210
t
cGcTa

Figure 1 - ||

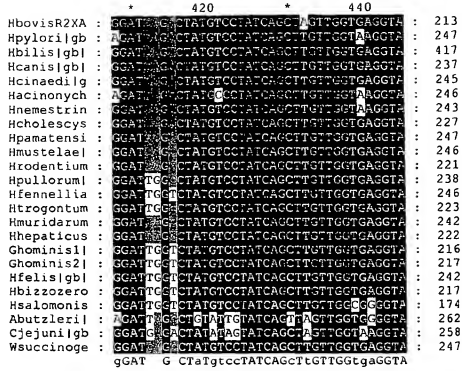

* 420 * 440
HbovisR2XA : GGATTGCGCTATGTCCTATCAGCCTAGTTGGTGAGGTA : 213
Hpylori|gb : AGATTGCGCTATGTCCTATCAGCTTGTTGGTAAGGTA : 247
Hbilis|gb| : GGATTGCGCTATGTCCTATCAGCTTGTTGGTGAGGTA : 417
Hcanis|gb| : GGATTGCGCTATGTCCTATCAGCTTGTTGGTGAGGTA : 237
Hcinaedi|g : GGATTGCGCTATGTCCTATCAGCTTGTTGGTGAGGTA : 245
Hacinonych : AGATTGCGCTATGCCCTATCAGCTTGTTGGTAAGGTA : 246
Hnemestrin : GGATTGCGCTATGTCCTATCAGCTTGTTGGTAAGGTA : 243
Hcholescys : GGATTGCGCTATGTCCTATCAGCTTGTTGGTGAGGTA : 227
Hpamatensi : GGATTGCGCTATGTCCTATCAGCTTGTTGGTGAGGTA : 247
Hmustelae| : GGATTGCGCTATGTCCTATCAGCTTGTTGGTGAGGTA : 246
Hrodentium : GGATTGCGCTATGTCCTATCAGCTTGTTGGTGAGGTA : 221
Hpulloruml : GGATTGCGCTATGTCCTATCAGCTTGTTGGTGAGGTA : 238
Hfennellia : GGATTGCGCTATGTCCTATCAGCTTGTTGGTGAGGTA : 246
Htrogontum : GGATTGCGCTATGTCCTATCAGCTTGTTGGTGAGGTA : 223
Hmuridarum : GGATTGCGCTATGTCCTATCAGCTTGTTGGTGAGGTA : 242
Hhepaticus : GGATTGCGCTATGTCCTATCAGCTTGTTGGTGAGGTA : 222
Ghominis1| : GGATTGCGCTATGTCCTATCAGCTTGTTGGTGAGGTA : 216
Ghominis2| : GGATTGCGCTATGTCCTATCAGCTTGTTGGTGAGGTA : 217
Hfelis|gb| : GGATTGCGCTATGTCCTATCAGCTTGTTGGTGAGGTA : 242
Hbizzozero : GGATTGCGCTATGTCCTATCAGCTTGTTGGTGAGGTA : 217
Hsalomonis : GGATTGCGCTATGTCCTATCAGCTTGTTGGCGCGGTA : 174
Abutzleri| : AGATTGCGCTGTATGTATCAGTTAGTTGGTGCGGTA : 262
Cjejuni|gb : GGATGGCGCTATAAGTATCAGCTAGTTGGTAAGGTA : 258
Wsuccinoge : GGATTGCGCTATGTCCTATCAGCTTGTTGGTGAGGTA : 247
gGAT G CTaTgtccTATCAGcTtGTTGGtgaGGTA

Figure 1 - 12

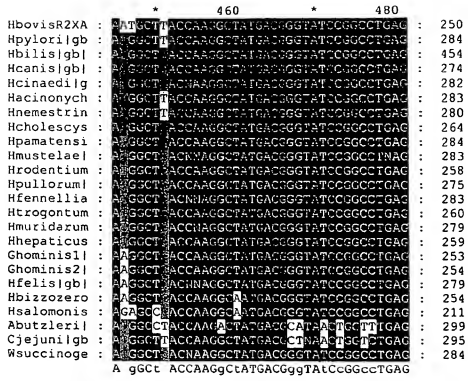

* 460 * 480
HbovisR2XA : 250
Hpylori|gb : 284
Hbilis|gb| : 454
Hcanis|gb| : 274
Hcinaedi|g : 282
Hacinonych : 283
Hnemestrin : 280
Hcholecys : 264
Hpamatensi : 284
Hmustelae| : 283
Hrodentium : 258
Hpullorum| : 275
Hfennellia : 283
Htrogontum : 260
Hmuridarum : 279
Hhepaticus : 259
Ghominis1| : 253
Ghominis2| : 254
Hfelis|gb| : 279
Hbizzozero : 254
Hsalomonis : 211
Abutzleri| : 299
Cjejuni|gb : 295
Wsuccinoge : 284
A gGCt ACCAAGgCtATGACGggTAtCcGGccTGAG

Figure 1 - 13

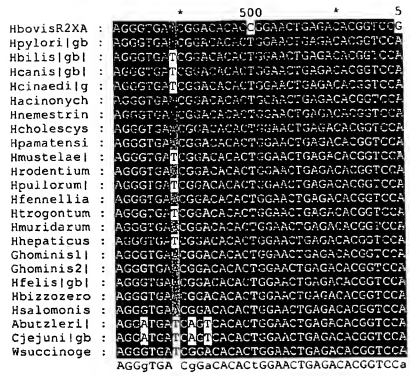
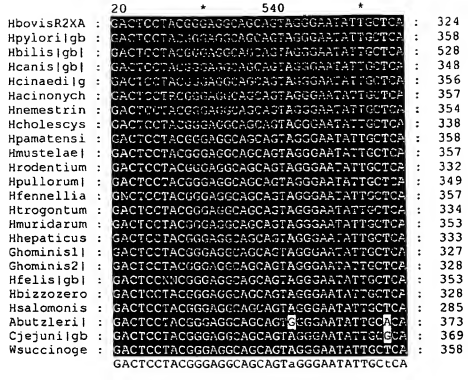

* 500 * 5
HbovisR2XA : AGGGTGAAGGGACACACGGAACTGAGACACGGTCCG : 287
Hpylori|gb : AGGGTGAAGGGACACACTGGAACTGAGACACGGTCCA : 321
Hbilis|gb| : AGGGTGATGGGACACACTGGAACTGAGACACGGTCCA : 491
Hcanis|gb| : AGGGTGATGGGACACACTGGAACTGAGACACGGTCCA : 311
Hcinaedi|g : AGGGTGATGGGACACACTGGAACTGAGACACGGTCCA : 319
Hacinonych : AGGGTGAAGGGACACACTGGAACTGAGACACGGTCCA : 320
Hnemestrin : AGGGTGAAGGGACACACTGGAACTGAGACACGGTCCA : 317
Hcholecys : AGGGTGAAGGGACACACTGGAACTGAGACACGGTCCA : 301
Hpamatensi : AGGGTGAAGGGACACACTGGAACTGAGACACGGTCCA : 321
Hmustelae| : AGGGTGATGGGACACACTGGAACTGAGACACGGTCCA : 320
Hrodentium : AGGGTGAAGGGACACACTGGAACTGAGACACGGTCCA : 295
Hpuilorum| : AGGGTGATGGGACACACTGGAACTGAGACACGGTCCA : 312
Hfennellia : AGGGTGAAGGGACACACTGGAACTGAGACACGGTCCA : 320
Htrogontum : AGGGTGATGGGACACACTGGAACTGAGACACGGTCCA : 297
Hmuridarum : AGGGTGAAGGGACACACTGGAACTGAGACACGGTCCA : 316
Hhepaticus : AGGGTGATGGGACACACTGGAACTGAGACACGGTCCA : 296
Ghominis1| : AGGGTGAAGGGACACACTGGAACTGAGACACGGTCCA : 290
Ghominis2| : AGGGTGAAGGGACACACTGGAACTGAGACACGGTCCA : 291
Hfelis|gb| : AGGGTGAAGGGACACACTGGAACTGAGACACGGTCCA : 316
Hbizzozero : AGGGTGAAGGGACACACTGGAACTGAGACACGGTCCA : 291
Hsalomonis : AGGGTGAAGGGACACACTGGAACTGAGACACGGTCCA : 248
Abutzleri| : AGGATGATGGAGTCACACTGGAACTGAGACACGGTCCA : 336
Cjejuni|gb : AGGATGATGGAGTCACACTGGAACTGAGACACGGTCCA : 332
Wsuccinoge : AGGGTGATGGGACACACTGGAACTGAGACACGGTCCA : 321
AGGgTGA CgGaCACACtGGAACTGAGACACGGTCCa

Figure 1 - 14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HbovisR2XA : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 324
Hpylori|gb : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 358
Hbilis|gb| : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 528
Hcanis|gb| : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 348
Hcinaedi|g : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 356
Hacinonych : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 357
Hnemestrin : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 354
Hcholecys : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 338
Hpamatensi : CACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 358
Hmustelae| : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 357
Hrodentium : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 332
Hpullorum| : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 349
Hfennellia : GNCTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 357
Htrogontum : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 334
Hmuridarum : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 353
Hhepaticus : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 333
Ghominis1| : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 327
Ghominis2| : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 328
Hfelis|gb| : GACTCCNNCGGGAGGCAGCAGTAGGGAATATTGCTCA : 353
Hbizzozero : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 328
Hsalomonis : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 285
Abutzleri| : GACTCCTACGGGAGGCAGCAGTGGGGAATATTGCGCA : 373
Cjejuni|gb : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCGCA : 369
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Figure 1 – 15

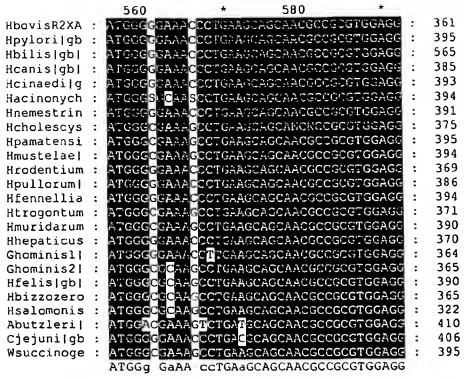
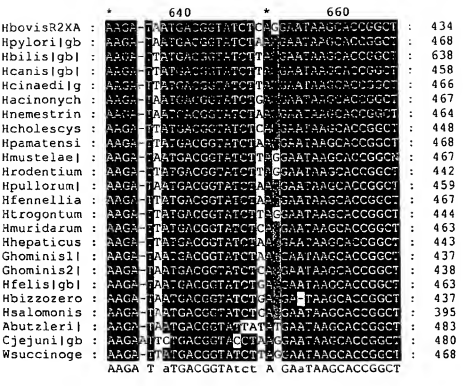

560
580
HbovisR2XA : ATGGGGGAAACCGTGAAGCAGCAACGCCGCGTGGAGG : 361
Hpylori|gb : ATGGGGGAAACCCTGAAGTAGCAACGCCGCGTTGAGG : 395
Hbilis|gb| : ATGGGGGAAACCCTGAAGTAGCAACGCCGCGTTGAGG : 565
Hcanis|gb| : ATGGGGGAAACCCTGAAGCAGCAACGCCGCGTTGAGG : 385
Hcinaedi|g : ATGGGGGAAACCCTGAAGCAGCAACGCCGCGTTGAGG : 393
Hacinonych : ATGGGSGCAASCCTGAAGCAGCAACGCCGCGTTGAGG : 394
Hnemestrin : ATGGGGGAAACCGTGAAGCAGCAACGCCGCGTTGAGG : 391
Hcholecys : ATGGGGGAAACCCTGAAGCAGCAACGCCGCGTTGAGG : 375
Hpamatensi : ATGGGGGAAACCCTGAAGCAGCAACGCCGCGTTGAGG : 395
Hmustelae| : ATGGGGGAAACCCTGAAGCAGCAACGCCGCGTTGAGG : 394
Hrodentium : ATGGGGGAAACCCTGAAGCAGCAACGCCGCGTTGAGG : 369
Hpullorum| : ATGGGGGAAACCCTGAAGCAGCAACGCCGCGTTGAGG : 386
Hfennellia : ATGGGGGAAACCCTGAAGCAGCAACGCCGCGTTGAGG : 394
Htrogontum : ATGGGGGAAACCCTGAAGCAGCAACGCCGCGTTGAGG : 371
Hmuridarum : ATGGGGGAAACCCTGAAGCAGCAACGCCGCGTTGAGG : 390
Hhepaticus : ATGGGGGAAACCCTGAAGCAGCAACGCCGCGTTGAGG : 370
Ghominis1| : ATGGGGGAAACCNTGAAGCAGCAACGCCGCGTTGAGG : 364
Ghominis2| : ATGGGGGCAACCCTGAAGCAGCAACGCCGCGTTGAGG : 365
Hfelis|gb| : ATGGGGGCAACCCTGAAGCAGCAACGCCGCGTTGAGG : 390
Hbizzozero : ATGGGGGCAACCCTGAAGCAGCAACGCCGCGTTGAGG : 365
Hsalomonis : ATGGGGGCAACCCTGAAGCAGCAACGCCGCGTTGAGG : 322
Abutzleri| : ATGGAGGAAAGTCTGATCAGCAACGCCGCGTTGAGG : 410
Cjejuni|gb : ATGGGGGAAACCCTGACCAGCAACGCCGCGTTGAGG : 406
Wsuccinoge : ATGGGGGAAACCCTGAAGCAGCAACGCCGCGTTGAGG : 395
ATGGg GaAA ccTGAaGCAGCAACGCCGCGTGGAGG

Figure 1 - 16


600
*
620
HbovisR2XA : ATGAAGGTTGTAGGATTGTAAACTCCTTTTGTGAGAG : 398
Hpylori|gb : ATGAAGGTTTTAGGATTGTAAACTCCTTTTGTGAGAC : 432
Hbilis|gb| : ATGAAGGTTTTAGGATTGTAAACTCCTTTTGTGAGAC : 602
Hcanis|gb| : ATGAAGGTTTTAGGATTGTAAACTCCTTTTGTGAGAC : 422
Hcinaedi|g : ATGAAGGTTTTAGGATTGTAAACTCCNTTTGTGAGAC : 430
Hacinonych : ATGAAGGTTTTAGGATTGTAAACTCCTTTTGTGAGAG : 431
Hnemestrin : ATGAAGGTTTTAGGATTGTAAACTCCTTTTGTGAGAG : 428
Hcholecys : ATGAAGGTTTTAGGATTGTAAACTCCTTTTGTGAGAG : 412
Hpamatensi : ATGAAGGTTTTAGGATTGTAAACTCCTTTTGTGAGAG : 432
Hmustelae| : ATGAAGGTTTTAGGATTGTAAACTCCTTTTGTGAGAG : 431
Hrodentium : ATGAAGGTTTTCGGATTGTAAACTCCTTTTGTGAGAG : 406
Hpullorum| : ATGAAGGTTTTCGGATTGTAAACTCCTTTTGTGAGAG : 423
Hfennellia : ATGAAGGTTTTAGGATTGTAAACTCCNNTTGTGAGAG : 431
Htrogontum : ATGAAGGTTTTAGGATTGTAAACTCCTTTTGCGAGAG : 408
Hmuridarum : ATGAAGGTTTTAGGATTGTAAACTCCTTTTGTGAGAG : 427
Hhepaticus : ATGAAGGTTTTAGGATTGTAAACTCCTTTTGTGAGAG : 407
Ghominis1| : ATGAAGGTTTTAGGATTGTAAACTCCTTTTGTGAGAG : 401
Ghominis2| : ATGAAGGTTTTAGGATTGTAAACTCCTTTTGTGAGAG : 402
Hfelis|gb| : ATGAAGGTTTTAGGATTGTAAACTCCTTTTGCGAGAG : 427
Hbizzozero : ATGAAGGTTTTAGGATTGTAAACTCCTTTTGCGAGAG : 402
Hsalomonis : ATGAAGGTTTTAGGATTGTAAACTCCTTTTGTGAGAG : 359
Abutzleri| : ATGACACATTTCGCTGCGTAAACTCCTTTTATATAAG : 447
Cjejuni|gb : ATGACACGTTTCGGAGCGTAAACTCCNNTTGCTAGGC : 443
Wsuccinoge : ATGAAGGTCTTCGGATTGTAAACTCCTTTTGTAGAG : 432
ATGAaggtttTaGGattGTAAACTCCTTTT T agaG

Figure 1 - 17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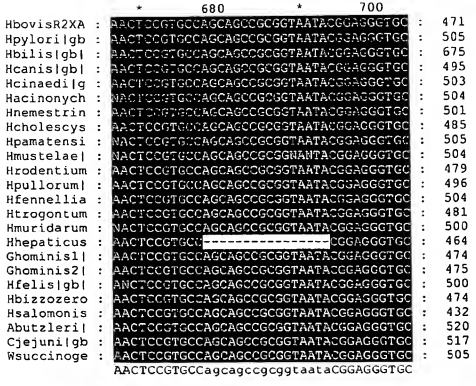
HbovisR2XA : AAGA-TTATGACGGTATCTAAGGAATAAGCACCGGCT : 434
Hpylori|gb : AAGA-TTATGACGGTATCTAAGGAATAAGCACCGGCT : 468
Hbilis|gb| : AAGA-TTATGACGGTATCTAAGGAATAAGCACCGGCT : 638
Hcanis|gb| : AAGA-TTATGACGGTATCTAAGGAATAAGCACCGGCT : 458
Hcinaedi|g : AAGA-TTATGACGGTATCTAAGGAATAAGCACCGGCT : 466
Hacinonych : AAGA-TAATGACGGTATCTGAGGAATAAGCACCGGCT : 467
Hnemestrin : AAGA-TAATGACGGTATCTAAGGAATAAGCACCGGCT : 464
Hcholescys : AAGA-TTATGACGGTATCTGAGGAATAAGCACCGGCT : 448
Hpamatensi : AAGA-TTATGACGGTATCTAAGGAATAAGCACCGGCT : 468
Hmustelae| : AAGA-TAATGACGGTATCTAAGGAATAAGCACCGGCN : 467
Hrodentium : AAGA-TTATGACGGTATCTAAGGAATAAGCACCGGCT : 442
Hpullorum| : AAGA-TAATGACGGTATCTAAGGAATAAGCACCGGCT : 459
Hfennellia : AAGA-TTATGACGGTATCTAAGGAATAAGCACCGGCT : 467
Htrogontum : AAGA-TTATGACGGTATCTAAGGAATAAGCACCGGCT : 444
Hmuridarum : AAGA-TTATGACGGTATCTAAGGAATAAGCACCGGCT : 463
Hhepaticus : AAGA-TTATGACGGTATCTAAGGAATAAGCACCGGCT : 443
Ghominisl| : AAGA-TAATGACGGTATCTAAGGAATAAGCACCGGCT : 437
Ghominis2| : AAGA-TAATGACGGTATCTAAGGAATAAGCACCGGCT : 438
Hfelis|gb| : AAGA-TAATGACGGTATCTAAGGAATAAGCACCGGCT : 463
Hbizzozero : AAGA-TAATGACGGTATCTGAGG-TAAGCACCGGCT : 437
Hsalomonis : AAGA-TTATGACGGTATCTAAGGAATAAGCACCGGCT : 395
Abutzleri| : AAGA-TAATGACGGTATTATGAATAAGCACCGGCT : 483
Cjejuni|gb : AAGAATTCAGACGGTACCTAAGGAATAAGCACCGGCT : 480
Wsuccinoge : AAGA-TTATGACGGTATCTAAGGAATAAGCACCGGCT : 468
AAGA T aTGACGGTAtct A GAaTAAGCACCGGCT

Figure 1 - 18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Hpylori|gb : AACTCCGTGCCAGCAGCCGCGGTAATACCGAAGGGTGC : 505
Hbilis|gb| : AACTCCGTGCCAGCAGCCGCGGTAATACCGAAGGGTGC : 675
Hcanis|gb| : AACTCCGTGCCAGCAGCCGCGGTAATACCGAAGGGTGC : 495
Hcinaedi|g : AACTCCGTGCCAGCAGCCGCGGTAATACCGAAGGGTGC : 503
Hacinonych : AACTCCGTGCCAGCAGCCGCGGTAATACCGAAGGGTGC : 504
Hnemestrin : AACTCCGTGCCAGCAGCCGCGGTAATACCGAAGGGTGC : 501
Hcholecys : AACTCCGTGCCAGCAGCCGCGGTAATACCGAAGGGTGC : 485
Hpamatensi : AACTCCGTGCCAGCAGCCGCGGTAATACCGAAGGGTGC : 505
Hmustelae| : AACTCCGTGCCAGCAGCCGCGGNANTACCGAAGGGTGC : 504
Hrodentium : AACTCCGTGCCAGCAGCCGCGGTAATACCGAAGGGTGC : 479
Hpullorum| : AACTCCGTGCCAGCAGCCGCGGTAATACCGAAGGGTGC : 496
Hfennellia : AACTCCGTGCCAGCAGCCGCGGTAATACNGAAGGGTGC : 504
Htrogontum : AACTCCGTGCCAGCAGCCGCGGTAATACCGAAGGGTGC : 481
Hmuridarum : AACTCCGTGCCAGCAGCCGCGGTAATACCGAAGGGTGC : 500
Hhepaticus : AACTCCGTGCC---------- CGAAGGGTGC : 464
Ghominis1| : AACTCCGTGCCAGCAGCCGCGGTAATACCGAAGGGTGC : 474
Ghominis2| : AACTCCGTGCCAGCAGCCGCGGTAATACCGAAGGGTGC : 475
Hfelis|gb| : ANCTCCGTGCCAGCAGCCGCGGTAATACCGAAGGGTGC : 500
Hbizzozero : AACTCCGTGCCAGCAGCCGCGGTAATACCGAAGGGTGC : 474
Hsalomonis : AACTCCGTGCCAGCAGCCGCGGTAATACCGAAGGGTGC : 432
Abutzleri| : AACTCCGTGCCAGCAGCCGCGGTAATACCGAAGGGTGC : 520
Cjejuni|gb : AACTCCGTGCCAGCAGCCGCGGTAATACCGAAGGGTGC : 517
Wsuccinoge : AACTCCGTGCCAGCAGCCGCGGTAATACCGAAGGGTGC : 505
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Figure 1 - 19

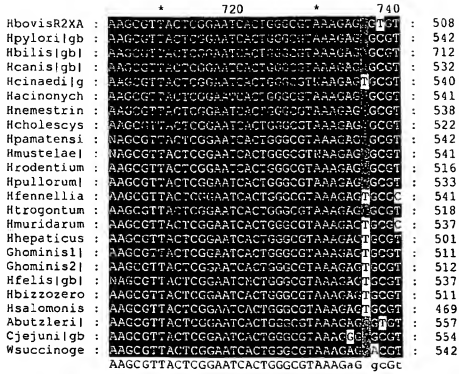
720
740
HbovisR2XA : AAGCGTTACTCGGAATCACTGGGCGTAAAGAG GTGT : 508
Hpylori|gb : AAGCGTTACTCGGAATCACTGGGCGTAAAGAG GCGT : 542
Hbilis|gb| : AAGCGTTACTCGGAATCACTGGGCGTAAAGAG GCGT : 712
Hcanis|gb| : AAGCGTTACTCGGAATCACTGGGCGTAAAGAG GCGT : 532
Hcinaedi|g : AAGCGTTACTCGGAATCACTGGGCGTAAAGAG GCGT : 540
Hacinonych : AAGCGTTACTCGGAATCACTGGGCGTAAAGAG GCGT : 541
Hnemestrin : AAGCGTTACTCGGAATCACTGGGCGTAAAGAG GCGT : 538
Hcholescys : AAGCGTTACTCGGAATCACTGGGCGTAAAGAG GCGT : 522
Hpamatensi : AAGCGTTACTCGGAATCACTGGGCGTAAAGAG GCGT : 542
Hmustelae| : AAGCGTTACTCGGAATCACTGGGCGTAAAGAG GCGT : 541
Hrodentium : AAGCGTTACTCGGAATCACTGGGCGTAAAGAG GCGT : 516
Hpullorum| : AAGCGTTACTCGGAATCACTGGGCGTAAAGAG GCGT : 533
Hfennellia : AAGCGTTACTCGGAATCACTGGGCGTAAAGAG GCGC : 541
Htrogontum : AAGCGTTACTCGGAATCACTGGGCGTAAAGAG GCGT : 518
Hmuridarum : AAGCGTTACTCGGAATCACTGGGCGTAAAGAG GCGC : 537
Hhepaticus : AAGCGTTACTCGGAATCACTGGGCGTAAAGAG GCGT : 501
Ghominis1| : AAGCGTTACTCGGAATCACTGGGCGTAAAGAG GCGT : 511
Ghominis2| : AAGCGTTACTCGGAATCACTGGGCGTAAAGAG GCGT : 512
Hfelis|gb| : AAGCGTTACTCGGAATCACTGGGCGTAAAGAG GCGT : 537
Hbizzozero : AAGCGTTACTCGGAATCACTGGGCGTAAAGAG GCGT : 511
Hsalomonis : AAGCGTTACTCGGAATCACTGGGCGTAAAGAG GCGT : 469
Abutzleri| : AAGCGTTACTCGGAATCACTGGGCGTAAAGAG GCGT : 557
Cjejuni|gb : AAGCGTTACTCGGAATCACTGGGCGTAAAGG GCGT : 554
Wsuccinoge : AAGCGTTACTCGGAATCACTGGGCGTAAAGAG ACGT : 542
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Figure 1 - 20

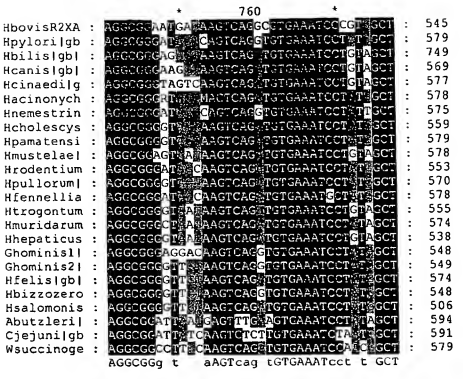
760
HbovisR2XA : AGGGGGAATGAAAGTCAGGCGTTGAAATGCCGTAGCT : 545
Hpylori|gb : AGGGGGCATGAAGTCAGGTGTGAAATCCTATAGCT : 579
Hbilis|gb| : AGGGGGCAGGAAGTCAGTGTGAAATCCTGTAGCT : 749
Hcanis|gb| : AGGGGGCAAGAAGTCAGTTTGAAATCCTGTAGCT : 569
Hcinaedi|g : AGGGGGCTAGTCAAGTCAGTGTGAAATCCTGTAGCT : 577
Hacinonych : AGGGGGCATTAAAACTCAGTGTGAAATCCTATAGCT : 578
Hnemestrin : AGGGGGCATTAAGCAGTCAGGTGTGAAATCCTATAGCT : 575
Hcholecys : AGGGGGCGTTAAAAGTCAGGTGTGAAATCCTATAGCT : 559
Hpamatensi : AGGGGGCGTTAAAAGTCAGGTGTGAAATCCTATAGCT : 579
Hmustelael : AGGGGGAGTTAATAAGTCAGGTGTGAAATCCTGTAGCT : 578
Hrodentium : AGGCGGGATTACAAGTCAGGTGTGAAATCCTATAGCT : 553
Hpullorum| : AGGCGGGCTTAAAAGTCAGGTGTGAAATCCTATAGCT : 570
Hfennellia : AGGCGGGCTTACAAGTCAGGTGTGAAATCCTGTAGCT : 578
Htrogontum : AGGCGGGCTTAAAAGTCAGGTGTGAAATCCTGTAGCT : 555
Hmuridarum : AGGCGGGCTTAAAAGTCAGGTGTGAAATCCTGTAGCT : 574
Hhepaticus : AGGCGGCCTTAAAAGTCAGGTGTGAAATCCTGTAGCT : 538
Ghominis1| : AGGCGGGAGGACAAGTCAGGTGTGAAATCCTATAGCT : 548
Ghominis2| : AGGCGGGATTAAAAGTCAGGTGTGAAATCCTATAGCT : 549
Hfelis|gb| : AGGCGGGCTTAAAGTCAGGTGTGAAATCCTGTAGCT : 574
Hbizzozero : AGGCGGGCTTAAAAGTCAGGTGTGAAATCCTATAGCT : 548
Hsalomonis : AGGCGGGCTTAAAAGTCAGGTGTGAAATCCTATAGCT : 506
Abutzleri| : AGGCGGATTAAAGAGTTGGAGTCAAATCCTATAGCT : 594
Cjejuni|gb : AGGGGGATTAACAAGTCTTGTGAAACCTATAGCT : 591
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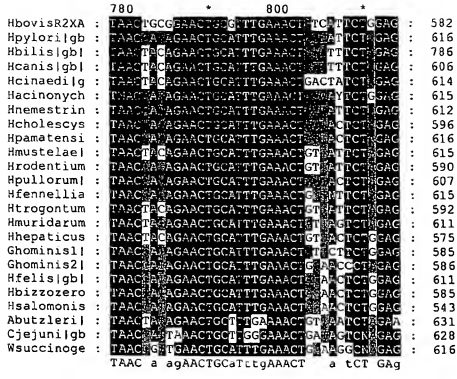
Figure 1 - 21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800
HbovisR2XA : 582
Hpylori|gb : 616
Hbilis|gb| : 786
Hcanis|gb| : 606
Hcinaedi|g : 614
Hacinonych : 615
Hnemestrin : 612
Hcholescys : 596
Hpamatensi : 616
Hmustelae| : 615
Hrodentium : 590
Hpullorum| : 607
Hfennellia : 615
Htrogontum : 592
Hmuridarum : 611
Hhepaticus : 575
Ghominis1| : 585
Ghominis2| : 586
Hfelis|gb| : 611
Hbizzozero : 585
Hsalomonis : 543
Abutzleri| : 631
Cjejuni|gb : 628
Wsuccinoge : 616
TAAC a agAACTGCaTttgAAACT a tCT GAg

Figure 1 - 22


820
*
840
*
HbovisR2XA : 619
Hpylori|gb : 653
Hbilis|gb| : 823
Hcanis|gb| : 643
Hcinaedi|g : 651
Hacinonych : 652
Hnemestrin : 649
Hcholescys : 633
Hpamatensi : 653
Hmustelae| : 652
Hrodentium : 627
Hpullorum| : 644
Hfennellia : 652
Htrogontum : 629
Hmuridarum : 648
Hhepaticus : 612
Ghominis1| : 622
Ghominis2| : 623
Hfelis|gb| : 648
Hbizzozero : 622
Hsalomonis : 580
Abutzleri| : 668
Cjejuni|gb : 665
Wsuccinoge : 653
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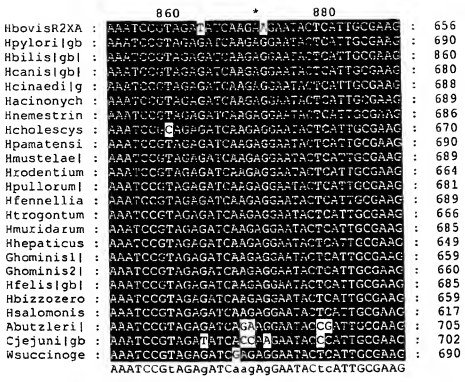
Figure 1 - 23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Hbilis|gb| : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAC : 860
Hcanis|gb| : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 680
Hcinaedi|g : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 688
Hacinonych : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 689
Hnemestrin : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 686
Hcholecys : AAATCCGCAGAGATCAAGAGGAATACTCATTGCGAAC : 670
Hpamatensi : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 690
Hmustelae| : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 689
Hrodentium : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 664
Hpullorum| : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 681
Hfennellia : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 689
Htrogontum : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 666
Hmuridarum : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 685
Hhepaticus : AAATCCGTAGAGATCAAGAGGAATACTCATTCCGAAC : 649
Ghominis1| : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 659
Ghominis2| : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAC : 660
Hfelis|gb| : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 685
Hbizzozero : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 659
Hsalomonis : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAC : 617
Abutzleri| : AAATCCGTAGAGATCAGAAGGAATACCGATTGCGAAG : 705
Cjejuni|gb : AAATCCGTAGATATCACGAGAATACGCATTGCGAAC : 702
Wsuccinoge : AAATCCGTAGAGATGCAGAGGAATACTCATTGCGAAG : 690
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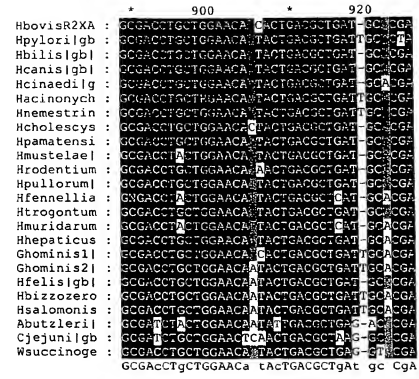
Figure 1 - 24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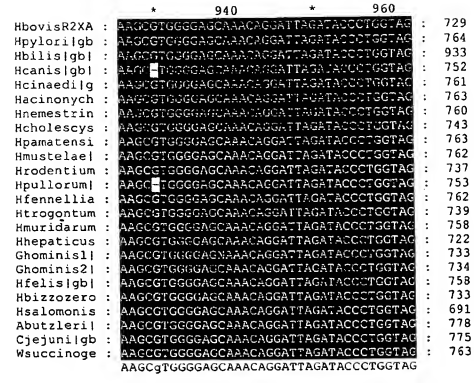
HbovisR2XA : 692
Hpylori|gb : 727
Hbilis|gb| : 896
Hcanis|gb| : 716
Hcinaedi|g : 724
Hacinonych : 726
Hnemestrin : 723
Hcholecys : 706
Hpamatensi : 726
Hmustelae| : 725
Hrodentium : 700
Hpullorum| : 717
Hfennellia : 725
Htrogontum : 702
Hmuridarum : 721
Hhepaticus : 685
Ghominis1| : 696
Ghominis2| : 697
Hfelis|gb| : 721
Hbizzozero : 696
Hsalomonis : 654
Abutzleri| : 741
Cjejuni|gb : 738
Wsuccinoge : 726
GCGAcCTgCTGGAACa tAcTGACGCTgAt gc CgA

Figure 1 - 25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HbovisR2XA : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 729
Hpylori|gb : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 764
Hbilis|gb| : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 933
Hcanis|gb| : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 752
Hcinaedi|g : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 761
Hacinonych : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 763
Hnemestrin : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 760
Hcholecys : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 743
Hpamatensi : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 763
Hmustelae| : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 762
Hrodentium : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 737
Hpullorum| : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 753
Hfennellia : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 762
Htrogontum : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 739
Hmuridarum : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 758
Hhepaticus : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 722
Ghominis1| : AAGCGTGGGGAGNAAACAGGATTAGATACCCTGGTAG : 733
Ghominis2| : AAGCGTGGGGAGCAAACAGGATTACATACCCTGGTAG : 734
Hfelis|gb| : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 758
Hbizzozero : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 733
Hsalomonis : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 691
Abutzleri| : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 778
Cjejuni|gb : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 775
Wsuccinoge : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 763
AAGCgTGGGGAGCAAACAGGATTAGATACCCTGGTAG

Figure 1 - 26

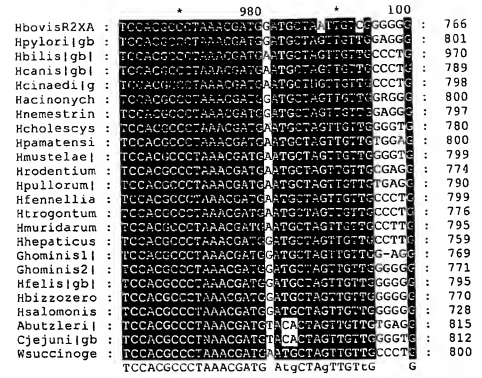

980
100
HbovisR2XA : 766
Hpylori|gb : 801
Hbilis|gb| : 970
Hcanis|gb| : 789
Hcinaedi|g : 798
Hacinonych : 800
Hnemestrin : 797
Hcholecys : 780
Hpamatensi : 800
Hmustelae| : 799
Hrodentium : 774
Hpullorum| : 790
Hfennellia : 799
Htrogontum : 776
Hmuridarum : 795
Hhepaticus : 759
Ghominis1| : 769
Ghominis2| : 771
Hfelis|gb| : 795
Hbizzozero : 770
Hsalomonis : 728
Abutzleri| : 815
Cjejuni|gb : 812
Wsuccinoge : 800
TCCACGCCCTAAACGATG AtgCTAgTTGTtG G

Figure 1 - 27


0
*
1020
*
HbovisR2XA : CTT-GTCTCCTGGCAATGCAGCTAACGCGTTAAGCA : 802
Hpylori|gb : CTTAGTCTCTCCAGTAATGCAGCTAACGCGTTAAGCA : 838
Hbilis|gb| : CTT-GTCAGGGCAGTAATGCAGCTAACGCGTTAAGCA : 1006
Hcanis|gb| : CTT-GTCAGGGCAGTAATGCAGCTAACGCGTTAAGCA : 825
Hcinaedi|g : CTT-GTCAGGGCAGTAATGCAGCTAACGCGTTAAGCA : 834
Hacinonych : CTTTGTCYYYCCAGTAATGCAGCTAACGCGTTAAGCA : 837
Hnemestrin : CTTAGTCTCTCCAGTAATGCAGCTAACGCGTTAAGCA : 834
Hcholecys : CTT-GTCACTCCAGTAATGCAGCTAACGCGTTAAGCA : 816
Hpamatensi : CTT-GTCTCTGCAGTAATGCAGCTAACGCGTTAAGCA : 836
Hmustelae| : CTT-GTCACTCCAGTAATGCAGCTAACGCGTTAAGCA : 835
Hrodentium : CTT-GTCCTTGCAGTAATGCAGCTAACGCGTTAAGCA : 810
Hpullorum| : CTT-GTCCTTGCAGTAATGCAGCTAACGCGTTAAGCA : 826
Hfennellia : CTC-GTCAGGGCAGTAATGCAGCTAACGCGTTAAGCA : 835
Htrogontum : CTT-GTCAGGGCAGTAATGCAGCTAACGCGTTAAGCA : 812
Hmuridarum : CTT-GTCAGGGCAGTAATGCAGCTAACGCGTTAAGCA : 831
Hhepaticus : CTT-GTCAGGGCAGTAATGCAGCTAACGCGTTAAGCA : 795
Ghominis1| : CTTTGTCTTTCCAGTAATGCAGCTAACGCGTTAAMNA : 806
Ghominis2| : CTTTGTCTCCCAGTAATGCAGCTAACGCGTTAAGCA : 808
Hfelis|gb| : CTT-GTCTCCCAGTAATGCAGCTAACGCGTTAAGCA : 831
Hbizzozero : CTTTGTCCCCCAGTAATGCAGCTAACGCGTTAAGCA : 807
Hsalomonis : CTTTGTCCCCCAGTAATGCAGCTAACGCGTTAAGCA : 765
Abutzleri| : CTC-GACCTTGCAGTAATGCAGCTAACGCGTTAAGTG : 851
Cjejuni|gb : CTA-GCCATCTCAGTAATGCAGCTAACGCGTTAAGTG : 848
Wsuccinoge : CTT-GTCAGGGCAGTAATGCAGCTAACGCGTTAAGCA : 836
CTt GtC CaGTAATGCAgcTAACgC TTAAGca

Figure 1 - 28


1040 * 1060 *
HbovisR2XA : TCCGCCTGGGGAGTACGATCGCAAGATTAAAACTCA : 839
Hpylori|gb : TCCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 875
Hbilis|gb| : TTCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 1043
Hcanis|gb| : TTCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 862
Hcinaedi|g : TTCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 871
Hacinonych : TCCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 874
Hnemestrin : TCCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 871
Hcholescys : TTCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 853
Hpamatensi : TTCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 873
Hmustelae| : TTCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 872
Hrodentium : TTCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 847
Hpullorum| : TTCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 863
Hfennellia : TTCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 872
Htrogontum : TTCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 849
Hmuridarum : TTCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 868
Hhepaticus : TTCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 832
Ghominis1| : TTC-GCCTGGGCAGTACGGTCGCAAGATTAAAACTCA : 842
Ghominis2| : TTCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 845
Hfelis|gb| : TTCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 868
Hbizzozero : TTCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 844
Hsalomonis : TTCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 802
Abutzleri| : TTACGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 888
Cjejuni|gb : TTACGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 885
Wsuccinoge : TTCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 873
T CGCCTGGGGAGTACGgTCGCAAGATTAAAACTCA

Figure 1 - 29

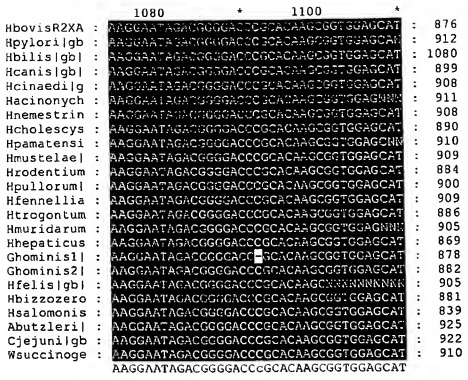
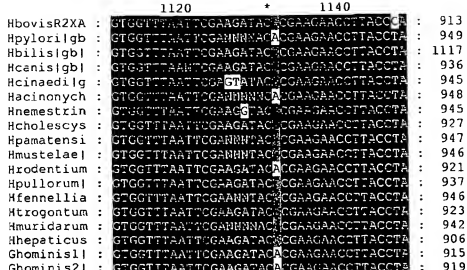

1080
1100
HbovisR2XA : AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT : 876
Hpylori|gb : AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT : 912
Hbilis|gb| : AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT : 1080
Hcanis|gb| : AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT : 899
Hcinaedi|g : AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT : 908
Hacinonych : AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT : 911
Hnemestrin : AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT : 908
Hcholecys : AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT : 890
Hpamatensi : AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCNN : 910
Hmustelae| : AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT : 909
Hrodentium : AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT : 884
Hpullorum| : AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT : 900
Hfennellia : AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT : 909
Htrogontum : AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT : 886
Hmuridarum : AAGGAATAGACGGGGACCCCCACAAGCGGTGGAGNNN : 905
Hhepaticus : AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT : 869
Ghominis1| : AAGGAATAGACGCGCAGC-GCACAAGCGGTGGAGCAT : 878
Ghominis2| : AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT : 882
Hfelis|gb| : AAGGAATAGACGGGGACCCGCACAAGCXXXNNNNNNN : 905
Hbizzozero : AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT : 881
Hsalomonis : AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT : 839
Abutzleri| : AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT : 925
Cjejuni|gb : AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT : 922
Wsuccinoge : AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT : 910
AAGGAATAGACGGGGACCcGCACAAGCGGTGGAGCAT

Figure 1 - 30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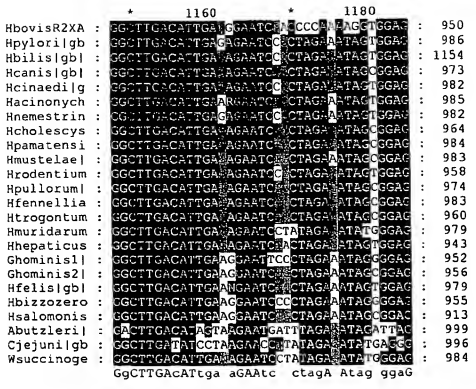
Hpylori|gb : GTGGTTTAATTCGAANNNAC ACGAAGAACCTTACCTA : 949
Hbilis|gb| : GTGATTTAATTCGAAGATAC CGAAGAACCTTACCTA : 1117
Hcanis|gb| : GTGATTTAATTCGAAGATAC CGAAGAACCTTACCTA : 936
Hcinaedi|g : GTGGTTTAATTCGATATAC CGAAGAACCTTACCTA : 945
Hacinonych : GTGGTTTAATTCGAANNNAC AGAAGAACCTTACCTA : 948
Hnemestrin : GTGGTTTAATTCGAAGGTAC CGAAGAACCTTACCTA : 945
Hcholecys : GTGGTTTAATTCGAAGATAC CGAAGAACCTTACCTA : 927
Hpamatensi : GTGCTTTAATTCGANNNTAC CGAAGAACCTTACCTA : 947
Hmustelae| : GTGGTTTAATTCGANNNTAC CGAAGAACCTTACCTA : 946
Hrodentium : GTGGTTTAATTCGAAGATAC ACGAAGAACCTTACCTA : 921
Hpullorum| : GTGGTTTAATTCGAAGATAC CGAAGAACCTTACCTA : 937
Hfennellia : GTGGTTTAATTCGAANNTAC CGAAGAACCTTACCTA : 946
Htrogontum : GTGGTTTAATTCGAAGATAC CGAAGAACCTTACCTA : 923
Hmuridarum : GTGGTTTAATTCGANNNNAC CGAAGAACCTTACCTA : 942
Hhepaticus : GTGGTTTAATTCGAAGATAC CGAAGAACCTTACCTA : 906
Ghominis1| : GTGGTTTAATTCGAAGATAC ACGAAGAACCTTACCTA : 915
Ghominis2| : GTGGTTTAATTCGAAGATAC ACGAAGAACCTTACCTA : 919
Hfelis|gb| : GTGGTTTAATTCGANNNNNN CGAAGAACCTTACCTA : 942
Hbizzozero : GTGGTTTAATTCGAAGATAC ACGAAGAACCTTACCTA : 918
Hsalomonis : GTGGTTTAATTCGATGGTAC ACGAAGAACCTTACCTA : 876
Abutzleri| : GTGGTTTAATTCGANNNNAC ACGAAGAACCTTACCTG : 962
Cjejuni|gb : GTGGTTTAATTCGAAGNTAC CGAAGAACCTTACCTG : 959
Wsuccinoge : GTGGTTTAATTCGANNNNAC CGAAGAACCTTACCTG : 947
GTGGTTTAATTCGAagaTAC CGAAGAACCTTACCta

Figure 1 - 31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1180
HbovisR2XA : 950
Hpylori|gb : 986
Hbilis|gb| : 1154
Hcanis|gb| : 973
Hcinaedi|g : 982
Hacinonych : 985
Hnemestrin : 982
Hcholecys : 964
Hpamatensi : 984
Hmustelae| : 983
Hrodentium : 958
Hpullorum| : 974
Hfennellia : 983
Htrogontum : 960
Hmuridarum : 979
Hhepaticus : 943
Ghominis1| : 952
Ghominis2| : 956
Hfelis|gb| : 979
Hbizzozero : 955
Hsalomonis : 913
Abutzleri| : 999
Cjejuni|gb : 996
Wsuccinoge : 984
GgCTTGAcATtga aGAAtc ctagA Atag ggaG

Figure 1 - 32

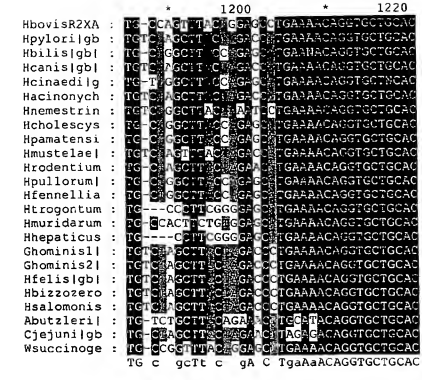
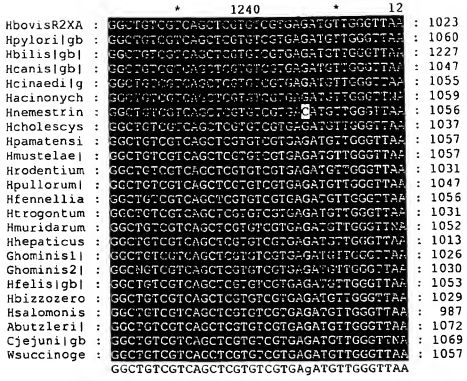

* 1200 * 1220
HbovisR2XA : TG-CCAGTTAGGGCGCTGAAAACAGGTGCTGCAC : 986
Hpylori|gb : TGTCAAGCTTCAGGCGCTGAAAACAGGTGCTGCAC : 1023
Hbilis|gb| : TGTCAGGCTTCAGGCGCTGAAAACAGGTGCTGCAC : 1190
Hcanis|gb| : TGTCAAGCTTCAGGCGCTGAAAACAGGTGCTGCAC : 1010
Hcinaedi|g : TG-TAGGCTTCAGGCGCTGAAAACAGGTGCTNCAC : 1018
Hacinonych : TGTCAAGCTTCAGGCGCTGAAAACAGGTGCTGCAC : 1022
Hnemestrin : TGTCAGGCTTAGGAGCTGAAAACAGGTGCTGCAC : 1019
Hcholescys : TGTCAGGCTTCAGGCGCTGAAAACAGGTGCTGCAC : 1000
Hpamatensi : TGTCAGGCTTCAGGCGCTGAAAACAGGTGCTGCAC : 1020
Hmustelae| : TGTCAAGCTTCAGGCGCTGAAAACACGTGCTGCAC : 1020
Hrodentium : TGTCAAGCTTCAGGCGCTGAAAACAGGTGCTGCAC : 994
Hpullorum| : TGTCAGGCTTCAGGCGCTGAAAACAGGTGCTGCAC : 1010
Hfennellia : TGTCAGGCTTCAGGCGCTGAAAACAGGTGCTGCAC : 1019
Htrogontum : TGT---GCTTTGGGCGCTGAAAACAGGTGCTGCAC : 994
Hmuridarum : TGTCACACTTCTGGCGCTGAAAACAGGTGCTGCAC : 1015
Hhepaticus : TGT----CTTTGGGCGCTGAAAACAGGTGCTGCAC : 976
Ghominis1| : TGTCAAGCTTCAGGCGCTGAAAACAGGTGCTGCAC : 989
Ghominis2| : TGTCAAGCTTCAGGCGCTGAAAACAGGTGCTGCAC : 993
Hfelis|gb| : TGTCAAGCTTCAGGCGCTGAAAACAGGTGCTGCAC : 1016
Hbizzozero : TGTCAAGCTTCAGGCGCTGAAAACAGGCTGCTGCAC : 992
Hsalomonis : TGTCAAGCTTCAGGCGCTGAAAACAGGTGCTGCAC : 950
Abutzleri| : TGTCTTGCTTCAGGAGCTGGGTACAGGTGCTGCAC : 1035
Cjejuni|gb : TGTCAAGCTTCAGGGGCTTACGCAGAGTGCTGCAC : 1032
Wsuccinoge : TGTCGCGCTTACAGGGCTGAAAACAGGTGCTGCAC : 1020
TG c gcTt c gA C TgaAaACAGGTGCTGCAC

Figure 1 – 33


* 1240 * 12
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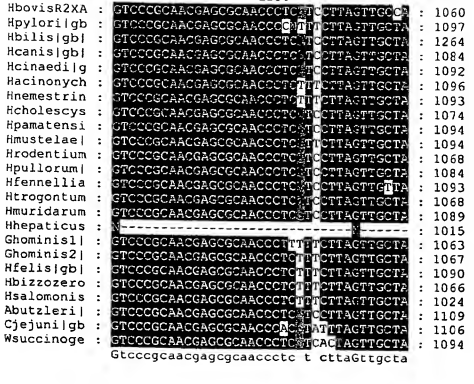
Hpylori|gb : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1060
Hbilis|gb| : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1227
Hcanis|gb| : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1047
Hcinaedi|g : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1055
Hacinonych : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1059
Hnemestrin : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1056
Hcholecys : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1037
Hpamatensi : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1057
Hmustelae| : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1057
Hrodentium : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1031
Hpullorum| : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1047
Hfennellia : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1056
Htrogontum : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1031
Hmuridarum : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1052
Hhepaticus : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1013
Ghominis1| : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1026
Ghominis2| : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1030
Hfelis|gb| : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1053
Hbizzozero : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1029
Hsalomonis : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 987
Abutzleri| : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1072
Cjejuni|gb : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1069
Wsuccinoge : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1057
GGCTGTCGTCAGCTCGTGTCGTGAgATGTTGGGTTAA

Figure 1 -34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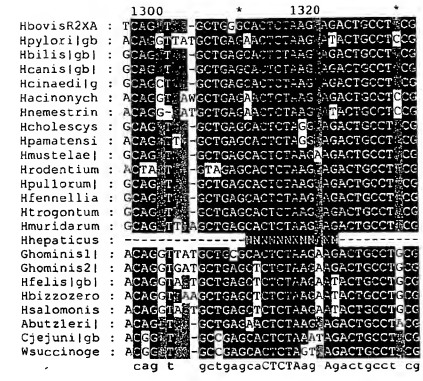
Hpylori|gb : GTCCCGCAACGAGCGCAACCCCGTTTCTTAGTTGCTA : 1097
Hbilis|gb| : GTCCCGCAACGAGCGCAACCCTCGTTCTTAGTTGCTA : 1264
Hcanis|gb| : GTCCCGCAACGAGCGCAACCCTCGTTCTTAGTTGCTA : 1084
Hcinaedi|g : GTCCCGCAACGAGCGCAACCCTCGTTCTTAGTTGCTA : 1092
Hacinonych : GTCCCGCAACGAGCGCAACCCTGTTTCTTAGTTGCTA : 1096
Hnemestrin : GTCCCGCAACGAGCGCAACCCTGTTTCTTAGTTGCTA : 1093
Hcholescys : GTCCCGCAACGAGCGCAACCCTCGTTCTTAGTTGCTA : 1074
Hpamatensi : GTCCCGCAACGAGCGCAACCCTCGTTCTTAGTTGCTA : 1094
Hmustelae| : GTCCCGCAACGAGCGCAACCCTCGTTCTTAGTTGCTA : 1094
Hrodentium : GTCCCGCAACGAGCGCAACCCTCGTTCTTAGTTGCTA : 1068
Hpullorum| : GTCCCGCAACGAGCGCAACCCTCGTTCTTAGTTGCTA : 1084
Hfennellia : GTCCCGCAACGAGCGCAACCCTCGTTCTTAGTTGTTA : 1093
Htrogontum : GTCCCGCAACGAGCGCAACCCTCGTTCTTAGTTGCTA : 1068
Hmuridarum : GTCCCGCAACGAGCGCAACCCTCGTTCTTAGTTGCTA : 1089
Hhepaticus : N---------- : 1015
Ghominis1| : GTCCCGCAACGAGCGCAACCCTTTTTCTTAGTTGCTA : 1063
Ghominis2| : GTCCCGCAACGAGCGCAACCCTGTTTCTTAGTTGCTA : 1067
Hfelis|gb| : GTCCCGCAACGAGCGCAACCCTCGTTCTTAGTTGCTA : 1090
Hbizzozero : GTCCCGCAACGAGCGCAACCCTCGTTCTTAGTTGCTA : 1066
Hsalomonis : GTCCCGCAACGAGCGCAACCCTCGTTCTTAGTTGCTA : 1024
Abutzleri| : GTCCCGCAACGAGCGCAACCCTCGTTCTTAGTTGCTA : 1109
Cjejuni|gb : GTCCCGCAACGAGCGCAACCCACGTTATTTAGTTGCTA : 1106
Wsuccinoge : GTCCCGCAACGAGCGCAACCCTCGTCACTAGTTGCTA : 1094
Gtcccgcaacgagcgcaaccctc t cttaGttgcta

Figure 1 ~ 35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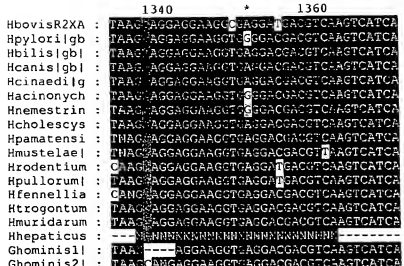
Hpylori|gb : ACAGGTTATGCTGAGAACTCTAAGATTACTGCCTCCG : 1134
Hbilis|gb| : GCAGTTG-GCTGAGGACTCTAAGAGACTGCCTTCG : 1300
Hcanis|gb| : GCAGTTG-GCTGAGCACTCTAAGAGACTGCCTTCG : 1120
Hcinaedi|g : GCACCTG-GCTGAGCACTCTAAGAGACTGCCTTCG : 1128
Hacinonych : ACACGTAWGCTGAGAACTCTAAGAGACTGCCTCCG : 1133
Hnemestrin : ACAGG-TATGCTGAGAACTCTAAGTTACTGCCTCCG : 1129
Hcholecys : GCAGTTG-GCTGAGCACTCTAGCAGACTGCCTTCG : 1110
Hpamatensi : ACAGTTG-GCTGAGCACTCTAGCAGACTGCCTTCG : 1130
Hmustelae| : GCAGTTG-GCTGAGCACTCTAAGAGAGTGCCTTCG : 1130
Hrodentium : ACTATTG-GTAGAGCACTCTAAGAGACTGCCTTCG : 1104
Hpullorum| : GCAGTTG-GCTGAGCACTCTAAGAGACTGCCTTCG : 1120
Hfennellia : CCAGTTG-GCTGAGCACTCTAAGAGACTGCCTTCG : 1129
Htrogontum : CCAGTTG-GCTGAGCACTCTAAGAGACTGCCTTCG : 1104
Hmuridarum : GCAGTTGAGCTGAGCACTCTAAGAGACTGCCTTCG : 1126
Hhepaticus : ----------HNNNNNNNNHNM---------- : 1027
Ghominis1| : ACAGGTTATGCTGCGCACTCTAAGAAGACTGCCTGCG : 1100
Ghominis2| : ACAGGTGATGCTGAGCTCTCTAAGAAGACTGCCTGCG : 1104
Hfelis|gb| : ACAGGTAGTGCTGAGCTCTCTAAGAATACTGCCTGCG : 1127
Hbizzozero : ACAGGTAAGCTGAGCTCTCTAAGAATACTGCCTGCG : 1103
Hsalomonis : ACAGGTAGTGCTGAGGTCTCTAAGAATACTGCCTGCG : 1061
Abutzleri| : ACAGTTG-GCTGAGAACTCTAAGAGACTGCCTACG : 1145
Cjejuni|gb : ACGGTTG-GCCGAGCACTCTAAATAGACTGCCTACG : 1142
Wsuccinoge : ACGGTTG-GCCGAGCACTCTAGTAGACTGCCTTCG : 1130
cag t gctgagcaCTCTAag Agactgcct cg

Figure 1 - 36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1360
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Hpylori|gb : TAAGTAGGAGGAAGGTGGGGACGACGTCAAGTCATCA : 1171
Hbilis|gb| : TAAGTAGGAGGAAGGTGAGGACGACGTCAAGTCATCA : 1337
Hcanis|gb| : TAAGCAGGAGGAAGCTGAGGACGACGTCAAGTCATCA : 1157
Hcinaedi|g : TAAGCAGGAGGAAGGTGAGGACGACGTCAAGTCATCA : 1165
Hacinonych : TAAGCAGGAGGAAGTGGGGACGACGTCAAGTCATCA : 1170
Hnemestrin : TAAGCAGGAGGAAGGTGGGACGACGTCAAGTCATCA : 1166
Hcholescys : TAAGCAGGAGGAAGCTGAGGACGACGTCAAGTCATCA : 1147
Hpamatensi : TNAGCAGGAGGAAGCTGAGGACGACGTCAAGTCATCA : 1167
Hmustelae| : TNACCAGGAGGAAGGTGAGGACGACGTTAAGTCATCA : 1167
Hrodentium : CAAGCAGGAGGAAGCTGAGGATGACGTCAAGTCATCA : 1141
Hpullorum| : TAAGCAGGAGGAAGCTGAGGATGACGTCAAGTCATCA : 1157
Hfennellia : CANGCAGGAGGAACGTGAGGACGACGTCAAGTCATCA : 1166
Htrogontum : TAAGCAGGAGGAAGCTGAGGACGACGTCAAGTCATCA : 1141
Hmuridarum : TAAGCAGGAGGAAGCTGAGGACGACGTCAAGTCATCA : 1163
Hhepaticus : ---CNNNNKKNNNKNNXNNNXNNNNNHNE-------- : 1053
Ghominis1| : TAAACT----AGGAAGCTGAGGACGACGTCAAGTCATCA : 1133
Ghominis2| : TAAGCAAGAGGAAGCTGAGGACGACGTCAAGTCATCA : 1141
Hfelis|gb| : TAAGCAGGAGGAAGCTGAGGACGACGTCAAGTCATCA : 1164
Hbizzozero : TAAGCAGGAGGAAGCTGAGGACGACGTCAAGTCATCA : 1140
Hsalomonis : TAAGCAGGAGGAAGGTGAGGACGACGTTAAGTCATCA : 1098
Abutzleri| : CAAGCTAGGAGGAAGCTCAGGATGACGTCAAGTCATCA : 1182
Cjejuni|gb : TNAGCAGGAGGAAGGTGTGGACGACGTCAAGTCATCA : 1179
Wsuccinoge : CAAGCAGGAGGAAGCTGAGGACGACGTCAAGTCATCA : 1167
taaG aggAGGAAGGtGaGGAcGACGTcAagtcatca

Figure 1 - 37

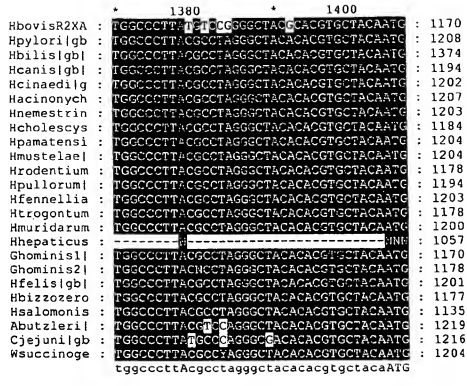

* 1380 * 1400
HbovisR2XA : TGGCCCTTACGCCTAGGGCTACACGCACGTGCTACAATG : 1170
Hpylori|gb : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1208
Hbilis|gb| : TGGCCCTTACGCCTAGGGCTACACACGTGGTACAATG : 1374
Hcanis|gb| : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1194
Hcinaedi|g : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1202
Hacinonych : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1207
Hnemestrin : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1203
Hcholecys : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1184
Hpamatensi : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1204
Hmustelae| : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1204
Hrodentium : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1178
Hpullorum| : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1194
Hfennellia : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1203
Htrogontum : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1178
Hmuridarum : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1200
Hhepaticus : --------G---------- : 1057
Ghominis1| : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1170
Ghominis2| : TGGCCCTTACNCCTAGGGCTACACACGTGCTACAATG : 1178
Hfelis|gb| : TGGCCCTTACGCCTAGGGCTACACACGTGGTACAATG : 1201
Hbizzozero : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1177
Hsalomonis : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1135
Abutzleri| : TGGCCCTTACGTGCAGGGCTACACACGTGCTACAATG : 1219
Cjejuni|gb : TGGCCCTTATGCCGAGGGCGACACACGTGCTACAATG : 1216
Wsuccinoge : TGGCCGTTACGCCYAGGGCTACACACGTGCTACAATG : 1204
tggcccttAcgcctagggctacacacgtgctacaATG

Figure 1 - 38

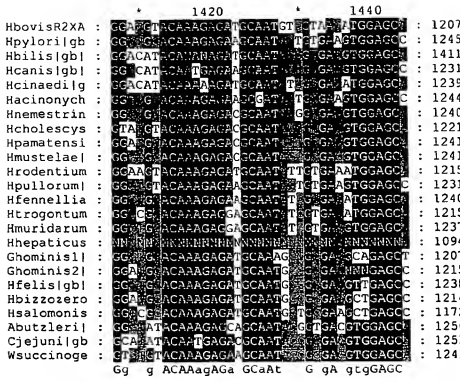

1420
1440
HbovisR2XA : 1207
Hpylori|gb| : 1245
Hbilis|gb| : 1411
Hcanis|gb| : 1231
Hcinaedi|g : 1239
Hacinonych : 1244
Hnemestrin : 1240
Hcholecys : 1221
Hpamatensi : 1241
Hmustelae| : 1241
Hrodentium : 1215
Hpullorum| : 1231
Hfennellia : 1240
Htrogontum : 1215
Hmuridarum : 1237
Hhepaticus : 1094
Ghominis1| : 1207
Ghominis2| : 1215
Hfelis|gb| : 1238
Hbizzozero : 1214
Hsalomonis : 1172
Abutzleri| : 1256
Cjejuni|gb : 1253
Wsuccinoge : 1241

Figure 1 - 39

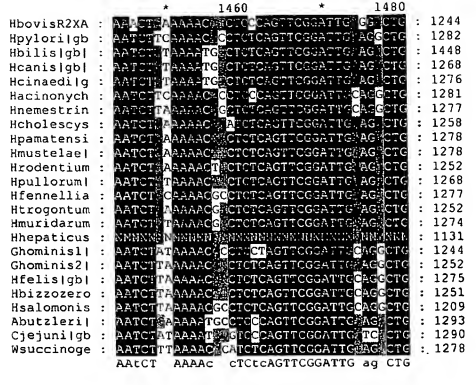

* 1460 * 1480
HbovisR2XA : 1244
Hpylori|gb : 1282
Hbilis|gb| : 1448
Hcanis|gb| : 1268
Hcinaedi|g : 1276
Hacinonych : 1281
Hnemestrin : 1277
Hcholescys : 1258
Hpamatensi : 1278
Hmustelae| : 1278
Hrodentium : 1252
Hpullorum| : 1268
Hfennellia : 1277
Htrogontum : 1252
Hmuridarum : 1274
Hhepaticus : 1131
Ghominis1| : 1244
Ghominis2| : 1252
Hfelis|gb| : 1275
Hbizzozero : 1251
Hsalomonis : 1209
Abutzleri| : 1293
Cjejuni|gb : 1290
Wsuccinoge : 1278
AAtCT AAAAc cTCtcAGTTCGGATTG ag CTG

Figure 1 - 40

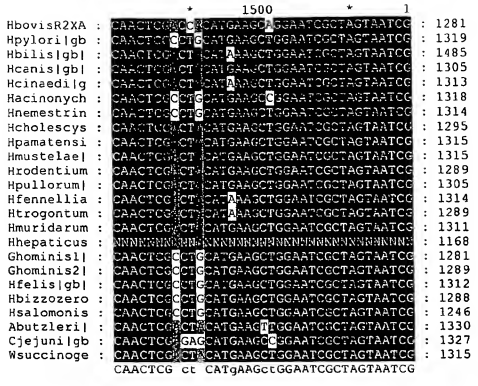

* 1500 * 1
HbovisR2XA : CAACTCGCCG CATGAAGCAG GAATCGCTAG TAATCG : 1281
Hpylori|gb : CAACTCGCGT GCATGAAGCT GGAATCGCTA GTAATCG : 1319
Hbilis|gb| : CAACTCGCCT GCATGAAGCT GGAATCGCTA GTAATCG : 1485
Hcanis|gb| : CAACTCGCCT GCATGAAGCT GGAATCGCTA GTAATCG : 1305
Hcinaedi|g : CAACTCGCCT GCATGAAGCT GGAATCGCTA GTAATCG : 1313
Hacinonych : CAACTCGCCG CATGCATGAAGCG GGAATCGCTA GTAATCG : 1318
Hnemestrin : CAACTCGCCG CATGCATGAAGCT GGAATCGCTA GTAATCG : 1314
Hcholecys : CAACTCGCCT GCATGAAGCT GGAATCGCTA GTAATCG : 1295
Hpamatensi : CAACTCGCCT GCATGAAGCT GGAATCGCTA GTAATCG : 1315
Hmustelae| : CAACTCGCCT GCATGAAGCT GGAATCGCTA GTAATCG : 1315
Hrodentium : CAACTCGCCT GCATGAAGCT GGAATCGCTA GTAATCG : 1289
Hpullorum| : CAACTCGCCT GCATGAAGCT GGAATCGCTA GTAATCG : 1305
Hfennellia : CAACTCGCCT GCATGAAGCT GGAATCGCTA GTAATCG : 1314
Htrogontum : CAACTCGCCT GCATGAAGCT GGAATCGCTA GTAATCG : 1289
Hmuridarum : CAACTCGCCT GCATGAAGCT GGAATCGCTA GTAATCG : 1311
Hhepaticus : NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNN : 1168
Ghominis1| : CAACTCGCCT GCATGAAGCT GGAATCGCTA GTAATCG : 1281
Ghominis2| : CAACTCGCCT GCATGAAGCT GGAATCGCTA GTAATCG : 1289
Hfelis|gb| : CAACTCGCCT GCATGAAGCT GGAATCGCTA GTAATCG : 1312
Hbizzozero : CAACTCGCCG CATGAAGCT GGAATCGCTA GTAATCG : 1288
Hsalomonis : CAACTCGCCT GCATGAAGCT GGAATCGCTA GTAATCG : 1246
Abutzleri| : CAACTCGCCT GCATGAAGCT GGAATCGCTA GTAATCG : 1330
Cjejuni|gb : CAACTCGCGAG CATGAAGCG GGAATCGCTA GTAATCG : 1327
Wsuccinoge : CAACTCGCCT GCATGAAGCT GGAATCGCTA GTAATCG : 1315
CAACTCG ct CATgAAGctGGAATCGCTAGTAATCG

Figure 1 - 4|

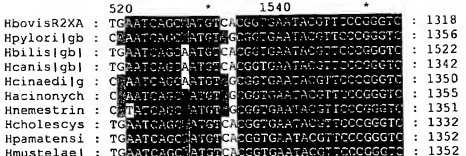

520 * 1540 *
HbovisR2XA : TGAATCAGCATGTCA CGGTGAATACGTTCCCGGGTC : 1318
Hpylori|gb : CGAATCAGCATGTAG CGGTGAATACGTTCCCGGGTC : 1356
Hbilis|gb| : TGAATCAGCATGTCA CGGTGAATACGTTCCCGGGTC : 1522
Hcanis|gb| : TGAATCAGCATGTCA CGGTGAATACGTTCCCGGGTC : 1342
Hcinaedi|g : CGAATCAGCATGTAG CGGTGAATACGTTCCCGGGTC : 1350
Hacinonych : CGAATCAGCATGTAG CGGTGAATACGTTCCCGGGTC : 1355
Hnemestrin : CGTATCAGCATGTAG CGGTGAATACGTTCCCGGGTC : 1351
Hcholecys : TGAATCAGCATGTCA CGGTGAATACGTTCCCGGGTC : 1332
Hpamatensi : TGAATCAGCATGTCA CGGTGAATACGTTCCCGGGTC : 1352
Hmustelae| : TGAATCAGCATGTCA CGGTGAATACGTTCCCGGGTC : 1352
Hrodentium : TGGATCAGCTATGCA CGGTGAATACGTTCCCGGGTC : 1326
Hpullorum| : CGAATCAGCATGTAG CGGTGAATACGTTCCCGGGTC : 1342
Hfennellia : CGAATCAGCAATGTG CGGTGAATACGTTCCCGGGTC : 1351
Htrogontum : CGAATCAGCAATGTG CGGTGAATACGTTCCCGGGTC : 1326
Hmuridarum : TGAATCAGCATGTCA CGGTGAATACGTCCCGGGTC : 1348
Hhepaticus : NNAATCAGCATGTCA CGGTGAATACGTTCCCGGGTN : 1205
Ghominis1| : CAAATCAGCTTATTG CGGTGAATACGTCCCGGGTC : 1318
Ghominis2| : CAAATCAGCGATGTG CGGTGAATACGTTCCCGGGTC : 1326
Hfelis|gb| : CGAATCAGCGATGTG CGGTGAATACGTTCCCGGGTC : 1349
Hbizzozero : CAAATCAGCGATGTG CGGTGAATACGTTCCCGGGTC : 1325
Hsalomonis : CAAATCAGCGATGTG CGGTGAATACGTCCCGGGTC : 1283
Abutzleri| : TGGATCAGCTATGCA CGGTGAATACGTTCCCGGGTC : 1367
Cjejuni|gb : TGGATCAGCGATGCA CGGTGAATACGTCCCGGGTC : 1364
Wsuccinoge : TGGATCAGCAATGCA CGGTGAATACGTCCCGGGTC : 1352
aATCAGC ATGt CGGTGAATACGTTCCCGGGTC

Figure 1 - 42

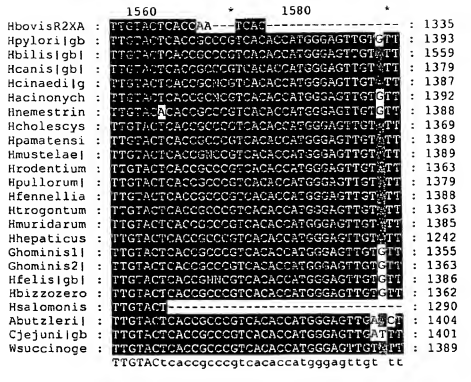

1560 * 1580 *
HbovisR2XA : TTGTAGTCACCAA---TCAG---------- : 1335
Hpylori|gb : TTGTAGTCACCGCCCGTCACACCATGGGAGTTGTGTT : 1393
Hbilis|gb| : TTGTAGTCACCGCCCGTCACACCATGGGAGTTGTGTT : 1559
Hcanis|gb| : TTGTAGTCACCGGMCGTNAACACATGGGAGTTGTATT : 1379
Hcinaedi|g : TTGTAGTCACCGCMCGTCACACCATGGGAGTTGTATT : 1387
Hacinonych : TTGTAGTCACCGCMCGTCACACCATGGGAGTTGTGTT : 1392
Hnemestrin : TTGTAGACACCGCCCGTCACACCATGGGAGTTGTGTT : 1388
Hcholecys : TTGTAGTCACCGCCCGTCACACCATGGGAGTTGTATT : 1369
Hpamatensi : TTGTAGTCACCGCCCGTCACACCATGGGAGTTGTATT : 1389
Hmustelae| : TTGTAGTCACCGMCGTCACACCATGGGAGTTGTATT : 1389
Hrodentium : TTGTAGTCACCGCCCGTCACACCATGGGAGTTGTATT : 1363
Hpullorum| : TTGTAGTCACCGCCCGTCACACCATGGGAGTTGTATT : 1379
Hfennellia : TTGTAGTCACCGCCCGTCACACCATGGGAGTTGTATT : 1388
Htrogontum : TTGTAGTCACCGCCCGTCACACCATGGGAGTTGTATT : 1363
Hmuridarum : TTGTAGTCACCGCCCGTCACACCATGGGAGTTGTATT : 1385
Hhepaticus : TTGTAGTCACCGCCCGTCACACCATGGGAGTTGTATT : 1242
Ghominis1| : TTGTAGTCACCGCCCGTCACACCATGGGAGTTGTGTT : 1355
Ghominis2| : TTGTAGTCACCGCCCGTCACACCATGGGAGTTGTGTT : 1363
Hfelis|gb| : TTGTAGTCACCGMMCGTCACACCATGGGAGTTGTGTT : 1386
Hbizzozero : TTGTAGTCACCGCCCGTCACACCATGGGAGTTGTGTT : 1362
Hsalomonis : TTGTAGT---------- : 1290
Abutzleri| : TTGTAGTCACCGCCCGTCACACCATGGGAGTTGTAGT : 1404
Cjejuni|gb : TTGTAGTCACCGCCCGTCACACCATGGGAGTTGTATT : 1401
Wsuccinoge : TTGTAGTCACCGCCCGTCACACCATGGGAGTTGTATT : 1389
TTGTACtcaccgcccgtcacaccatgggagttgt tt

Figure 1 - 43

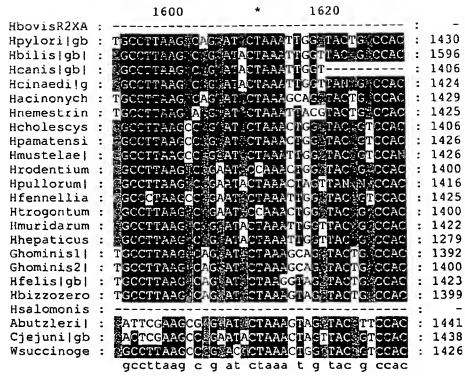

1600
*
1620
HbovisR2XA
Hpylori|gb
Hbilis|gb|
Hcanis|gb|
Hcinaedi|g
Hacinonych
Hnemestrin
Hcholecys
Hpamatensi
Hmustelae|
Hrodentium
Hpullorum|
Hfennellia
Htrogontum
Hmuridarum
Hhepaticus
Ghominis1|
Ghominis2|
Hfelis|gb|
Hbizzozero
Hsalomonis
Abutzleri|
Cjejuni|gb
Wsuccinoge
gccttaag c g at ctaaa t g tac g ccac

Figure 1 - 44

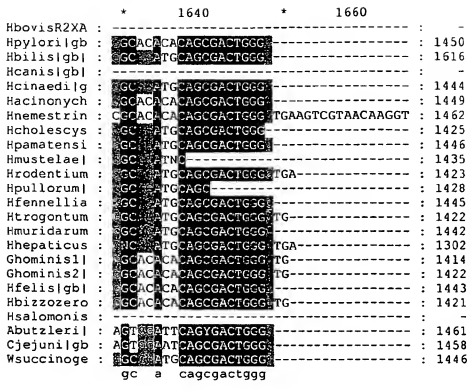

* 1640 * 1660
HbovisR2XA :
Hpylori|gb :
Hbilis|gb| :
Hcanis|gb| :
Hcinaedi|g :
Hacinonych :
Hnemestrin :
Hcholecys :
Hpamatensi :
Hmustelae| :
Hrodentium :
Hpullorum| :
Hfennellia :
Htrogontum :
Hmuridarum :
Hhepaticus :
Ghominis1| :
Ghominis2| :
Hfelis|gb| :
Hbizzozero :
Hsalomonis :
Abutzleri| :
Cjejuni|gb :
Wsuccinoge :
gc a cagcgactggg

Figure 1 - 45

```
HbovisR2XA : ---------- :    -
Hpylori|gb : ---------- :    -
Hbilis|gb| : ---------- :    -
Hcanis|gb| : ---------- :    -
Hcinaedi|g : ---------- :    -
Hacinonych : ---------- :    -
Hnemestrin : A--------- : 1463
Hcholescys : ---------- :    -
Hpamatensi : ---------- :    -
Hmustelae| : ---------- :    -
Hrodentium : ---------- :    -
Hpullorum| : ---------- :    -
Hfennellia : ---------- :    -
Htrogontum : ---------- :    -
Hmuridarum : ---------- :    -
Hhepaticus : ---------- :    -
Ghominis1| : ---------- :    -
Ghominis2| : ---------- :    -
Hfelis|gb| : ---------- :    -
Hbizzozero : ---------- :    -
Hsalomonis : ---------- :    -
Abutzleri| : ---------- :    -
Cjejuni|gb : ---------- :    -
Wsuccinoge : ---------- :    -
```

Figure 1 - 46

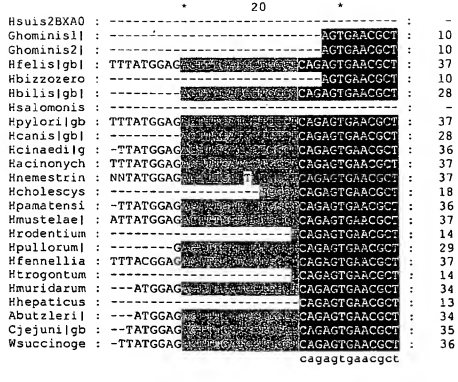

* 20 *
Hsuis2BXA0 : - -
Ghominis1| : AGTGAACGCT : 10
Ghominis2| : AGTGAACGCT : 10
Hfelis|gb| : TTTATGGAG CAGAGTGAACGCT : 37
Hbizzozero : AGTGAACGCT : 10
Hbilis|gb| : CAGAGTGAACGCT : 28
Hsalomonis : - -
Hpylori|gb : TTTATGGAG CAGAGTGAACGCT : 37
Hcanis|gb| : CAGAGTGAACGCT : 28
Hcinaedi|g : -TTATGGAG CAGAGTGAACGCT : 36
Hacinonych : TTTATGGAG CAGAGTGAACGCT : 37
Hnemestrin : NNTATGGAG CAGAGTGAACGCT : 37
Hcholescys : CAGAGTGAACGCT : 18
Hpamatensi : -TTATGGAG CAGAGTGAACGCT : 36
Hmustelae| : ATTATGGAG CAGAGTGAACGCT : 37
Hrodentium : CAGAGTGAACGCT : 14
Hpullorum| : CAGAGTGAACGCT : 29
Hfennellia : TTTACGGAG CAGAGTGAACGCT : 37
Htrogontum : CAGAGTGAACGCT : 14
Hmuridarum : ---ATGGAG CAGAGTGAACGCT : 34
Hhepaticus : CAGAGTGAACGCT : 13
Abutzleri| : ---ATGGAG CAGAGTGAACGCT : 34
Cjejuni|gb : --TATGGAG CAGAGTGAACGCT : 35
Wsuccinoge : -TTATGGAG CAGAGTGAACGCT : 36
cagagtgaacgct

Figure 2 - 1

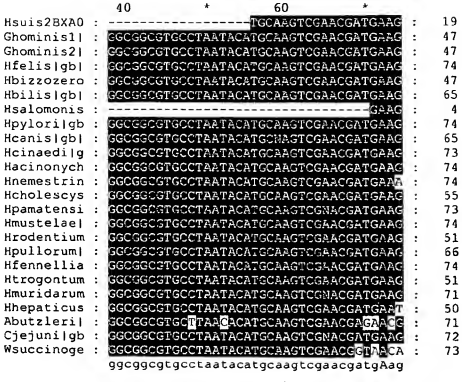

40 * 60 *
Hsuis2BXA0 : ----------TGCAAGTCGAACGATGAAG : 19
Ghominis1| : GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG : 47
Ghominis2| : GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG : 47
Hfelis|gb| : GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG : 74
Hbizzozero : GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG : 47
Hbilis|gb| : GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG : 65
Hsalomonis : ----------GAAG : 4
Hpylori|gb : GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG : 74
Hcanis|gb| : GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG : 65
Hcinaedi|g : GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG : 73
Hacinonych : GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG : 74
Hnemestrin : GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAA : 74
Hcholescys : GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG : 55
Hpamatensi : GGCGGCGTGCCTAATACATGCAAGTCGNACGATGAAG : 73
Hmustelae| : GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG : 74
Hrodentium : GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG : 51
Hpullorum| : GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG : 66
Hfennellia : GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG : 74
Htrogontum : GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG : 51
Hmuridarum : GGCGGCGTGCCTAATACATGCAAGTCGNACGATGAAG : 71
Hhepaticus : GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAT : 50
Abutzleri| : GGCGGCGTGCTTAACACATGCAAGTCGAACGAGAAGC : 71
Cjejuni|gb : GGCGGCGTGCCTAATACATGCAAGTCGNACGATGAAG : 72
Wsuccinoge : GGCGGCGTGCCTAATACATGCAAGTCGAACGTTACCA : 73
ggcggcgtgcctaatacatgcaagtcgaacgatgAag

Figure 2 -2


80 * 100 *
Hsuis2BXA0 : C--C-TAGCTTGCTAG---GTT--GATTAGTGGCGCA : 48
Ghominis1| : C--C-TAGCTTGCTAG----TT--GATTAGTGGCGCA : 75
Ghominis2| : C--C-TAGCTTGCTAG---GTG--GATTAGTGGCGCA : 76
Hfelis|gb| : C--C-TAGCTTGCTAG---GCG--GATTAGTGGCGCA : 103
Hbizzozero : C--C-TAGCTTGCTAG---GTG--GATTAGTGGCGCA : 76
Hbilis|gb| : CTGC-TAGCTTGCTAGAAGTG---GATTAGTGGCGCA : 98
Hsalomonis : C--C-TAGCTTGCTAG---GCG--GATTAGTGGCGCA : 33
Hpylori|gb : CTGC-TAGCTTGCTAGAGTGCT--GATTAGTGGCGCA : 108
Hcanis|gb| : CTTT-TAGCTTGCTAGAAGTG---GATTAGTGGCGCA : 98
Hcinaedi|g : CTTT-TAGCTTGCTAGAAGTG---GATTAGTGGCGCA : 106
Hacinonych : CTGC-TAGCTTGCTAGAA-GTG--GATTAGTGGCGCA : 107
Hnemestrin : CTCT-TAGCTTGC----ATGCT--GATTAGTGGCGCA : 104
Hcholescys : CTTT-TAGCTTGCTAGT-AGTG--GATTAGTGGCGCA : 88
Hpamatensi : CTCTCTAGCTTGCTAGAGAGTG--GATTAGTGGCGCA : 108
Hmustelae| : CTGC-TAGCTTGCTAGT-AGTG--GATTAGTGGCGCA : 107
Hrodentium : C--TCTAGCTTGCTAGAGTGG---GATTAGTGGCGCA : 82
Hpullorum| : C-TTCTAGCTTGCTAGAAGTG---GATTAGTGGCGCA : 99
Hfennellia : TCGC-TAGCTTGCTAGAGATG---GATTAGTGGCGCA : 107
Htrogontum : CTTT-TAGCTTGCTAGAAGTG---GATTAGTGGCGCA : 84
Hmuridarum : CTTT-TAGCTTGCTAGAAGTG---GATTAGTGGCGCA : 104
Hhepaticus : CTGC-TAGCTTGCTAGAAGTG---GATTAGTGGCGCA : 83
Abutzleri| : GATTATAGCTTGCTATTAATTGTCAGTAAGTGGCGCA : 108
Cjejuni|gb : C-TTCTAGCTTGCTAGAAGTG---GATTAGTGGCGCA : 105
Wsuccinoge : GGGTGTAGCTTGCTATTGCTGCT--GATGAGTGGCGCA : 108
c tAGCTTGCtag gattAGTGGCGCA

Figure 2 - 3

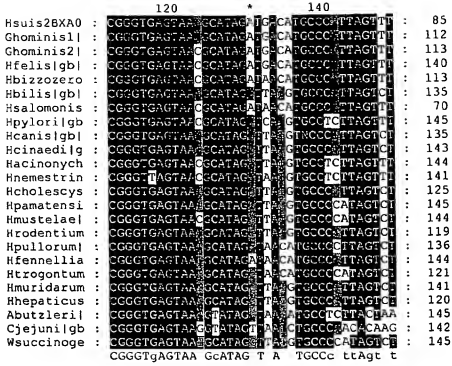

120
*
140
Hsuis2BXA0 : CGGGTGAGTAA GCATAG T A TGCCc TTAGT T : 85
Ghominis1| : CGGGTGAGTAA GCATAG T A TGCCc TTAGT T : 112
Ghominis2| : CGGGTGAGTAA GCATAG T A TGCCc TTAGT T : 113
Hfelis|gb| : CGGGTGAGTAA GCATAG T A TGCCc TTAGT T : 140
Hbizzozero : CGGGTGAGTAA GCATAG T A TGCCc TTAGT T : 113
Hbilis|gb| : CGGGTGAGTAA GCATAG T A TGCCc TTAGT C : 135
Hsalomonis : CGGGTGAGTAA GCATAG T A TGCCc TTAGT T : 70
Hpylori|gb : CGGGTGAGTAA GCATAG C T A TGCC TC TTAGT T : 145
Hcanis|gb| : CGGGTGAGTAA GCATAG T A TGCCc TTAGT C : 135
Hcinaedi|g : CGGGTGAGTAA GCATAG T A TGCCc TTAGT C : 143
Hacinonych : CGGGTGAGTAA GCATAG T A TGCC TC TTAGT T : 144
Hnemestrin : CGGGTTAGTAA GCATAG T A TGCC TC TTAGT T : 141
Hcholescys : CGGGTGAGTAA GCATAG T A TGCCc TTAGT C : 125
Hpamatensi : CGGGTGAGTAA GCATAG C T A TGCCC CATAGT C : 145
Hmustelae| : CGGGTGAGTAA GCATAG T A TGCCC CATAGT C : 144
Hrodentium : CGGGTGAGTAA GCATAG T A TGCCc TTAGT C : 119
Hpullorum| : CGGGTGAGTAA GCATAG T A TGCC TTAGC T : 136
Hfennellia : CGGGTGAGTAA GCATAG T A TGCCc TTAGT C : 144
Htrogontum : CGGGTGAGTAA GCATAG T A TGCC TGCCC CATAGT C : 121
Hmuridarum : CGGGTGAGTAA GCATAG T A TGCCc TTAGT C : 141
Hhepaticus : CGGGTGAGTAA GCATAG T A TGCCc TTAGT C : 120
Abutzleri| : CGGGTGAGTAA GCATAG T A TGCC TC TTAC AA : 145
Cjejuni|gb : CGGGTGAGTAA GCATAG T A TGCCc TAC CAAG : 142
Wsuccinoge : CGGGTGAGTAA GCATAG T A TGCCc CATAGT C : 145
CGGGTgAGTAA GcATAG T A TGCCc ttAgt t

Figure 2 - 4


160
180
Hsuis2BXA0 : 122
Ghominis1| : 149
Ghominis2| : 150
Hfelis|gb| : 177
Hbizzozero : 150
Hbilis|gb| : 172
Hsalomonis : 107
Hpylori|gb : 182
Hcanis|gb| : 172
Hcinaedi|g : 180
Hacinonych : 181
Hnemestrin : 178
Hcholescys : 162
Hpamatensi : 182
Hmustelae| : 181
Hrodentium : 156
Hpullorum| : 173
Hfennellia : 181
Htrogontum : 158
Hmuridarum : 178
Hhepaticus : 157
Abutzleri| : 182
Cjejuni|gb : 179
Wsuccinoge : 182
gGgAtAgCca T GAAA GgtgatTAATAC ATAc

Figure 2 - 5

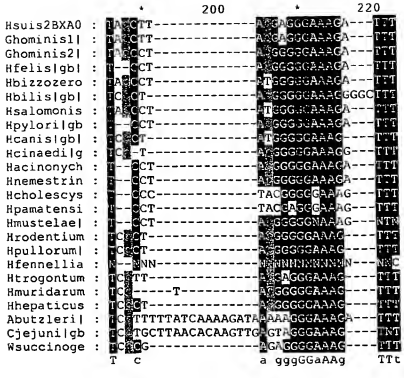

200
220
Hsuis2BXA0 : 143
Ghominis1| : 170
Ghominis2| : 171
Hfelis|gb| : 196
Hbizzozero : 171
Hbilis|gb| : 195
Hsalomonis : 128
Hpylori|gb : 201
Hcanis|gb| : 191
Hcinaedi|g : 199
Hacinonych : 200
Hnemestrin : 197
Hcholescys : 181
Hpamatensi : 201
Hmustelae| : 200
Hrodentium : 175
Hpullorum| : 192
Hfennellia : 200
Htrogontum : 177
Hmuridarum : 196
Hhepaticus : 176
Abutzleri| : 216
Cjejuni|gb : 212
Wsuccinoge : 201

Figure 2 - 6

```
                    *       240         *       26
Hsuis2BXA0  : ------------------------------------ :    -
Ghominis1|  : ------------------------------------ :    -
Ghominis2|  : ------------------------------------ :    -
Hfelis|gb|  : ------------------------------------ :    -
Hbizzozero  : ------------------------------------ :    -
Hbilis|gb|  : CAATAAAGAATTTCTCTTTTTAGTGCTTTGTGTTGTT :  232
Hsalomonis  : ------------------------------------ :    -
Hpylori|gb  : ------------------------------------ :    -
Hcanis|gb|  : ------------------------------------ :    -
Hcinaedi|g  : ------------------------------------ :    -
Hacinonych  : ------------------------------------ :    -
Hnemestrin  : ------------------------------------ :    -
Hcholescys  : ------------------------------------ :    -
Hpamatensi  : ------------------------------------ :    -
Hmustelae|  : ------------------------------------ :    -
Hrodentium  : ------------------------------------ :    -
Hpullorum|  : ------------------------------------ :    -
Hfennellia  : ------------------------------------ :    -
Htrogontum  : ------------------------------------ :    -
Hmuridarum  : ------------------------------------ :    -
Hhepaticus  : ------------------------------------ :    -
Abutzleri|  : ------------------------------------ :    -
Cjejuni|gb  : ------------------------------------ :    -
Wsuccinoge  : ------------------------------------ :    -
```

Figure 2 - 7

```
                0          *       280          *
Hsuis2BXA0  : ---------------------------------------- :    -
Ghominis1|  : ---------------------------------------- :    -
Ghominis2|  : ---------------------------------------- :    -
Hfelis|gb|  : ---------------------------------------- :    -
Hbizzozero  : ---------------------------------------- :    -
Hbilis|gb|  : GGCACAAAATTCTAGTATTTGGAATGAGAAATTGATG    :  269
Hsalomonis  : ---------------------------------------- :    -
Hpylori|gb  : ---------------------------------------- :    -
Hcanis|gb|  : ---------------------------------------- :    -
Hcinaedi|g  : ---------------------------------------- :    -
Hacinonych  : ---------------------------------------- :    -
Hnemestrin  : ---------------------------------------- :    -
Hcholescys  : ---------------------------------------- :    -
Hpamatensi  : ---------------------------------------- :    -
Hmustelae|  : ---------------------------------------- :    -
Hrodentium  : ---------------------------------------- :    -
Hpullorum|  : ---------------------------------------- :    -
Hfennellia  : ---------------------------------------- :    -
Htrogontum  : ---------------------------------------- :    -
Hmuridarum  : ---------------------------------------- :    -
Hhepaticus  : ---------------------------------------- :    -
Abutzleri|  : ---------------------------------------- :    -
Cjejuni|gb  : ---------------------------------------- :    -
Wsuccinoge  : ---------------------------------------- :    -
```

Figure 2 - 8

```
                  300          *          320          *
Hsuis2BXA0  : ------------------------------------------ :   -
Ghominis1|  : ------------------------------------------ :   -
Ghominis2|  : ------------------------------------------ :   -
Hfelis|gb|  : ------------------------------------------ :   -
Hbizzozero  : ------------------------------------------ :   -
Hbilis|gb|  : TTGTGAAGCAATTTGTGCGGAGACTAGACTTAGTGTC       :  306
Hsalomonis  : ------------------------------------------ :   -
Hpylori|gb  : ------------------------------------------ :   -
Hcanis|gb|  : ------------------------------------------ :   -
Hcinaedi|g  : ------------------------------------------ :   -
Hacinonych  : ------------------------------------------ :   -
Hnemestrin  : ------------------------------------------ :   -
Hcholescys  : ------------------------------------------ :   -
Hpametensi  : ------------------------------------------ :   -
Hmustelae|  : ------------------------------------------ :   -
Hrodentium  : ------------------------------------------ :   -
Hpullorum|  : ------------------------------------------ :   -
Hfennellia  : ------------------------------------------ :   -
Htrogontum  : ------------------------------------------ :   -
Hmuridarum  : ------------------------------------------ :   -
Hhepaticus  : ------------------------------------------ :   -
Abutzleri|  : ------------------------------------------ :   -
Cjejuni|gb  : ------------------------------------------ :   -
Wsuccinoge  : ------------------------------------------ :   -
```

Figure 2 - 9

```
                340          *          360          *
Hsuis2BXA0  : ------------------------------------ :    -
Ghominis1|  : ------------------------------------ :    -
Ghominis2|  : ------------------------------------ :    -
Hfelis|gb|  : ------------------------------------ :    -
Hbizzozero  : ------------------------------------ :    -
Hbilis|gb|  : TGTCGCACAAGCAAATTGCGAACTCATCGATTTATCG :  343
Hsalomonis  : ------------------------------------ :    -
Hpylori|gb  : ------------------------------------ :    -
Hcanis|gb|  : ------------------------------------ :    -
Hcinaedi|g  : ------------------------------------ :    -
Hacinonych  : ------------------------------------ :    -
Hnemestrin  : ------------------------------------ :    -
Hcholescys  : ------------------------------------ :    -
Hpamatensi  : ------------------------------------ :    -
Hmustelae|  : ------------------------------------ :    -
Hrodentium  : ------------------------------------ :    -
Hpullorum|  : ------------------------------------ :    -
Hfennellia  : ------------------------------------ :    -
Htrogontum  : ------------------------------------ :    -
Hmuridarum  : ------------------------------------ :    -
Hhepaticus  : ------------------------------------ :    -
Abutzleri|  : ------------------------------------ :    -
Cjejuni|gb  : ------------------------------------ :    -
Wsuccinoge  : ------------------------------------ :    -
```

Figure 2 - 10

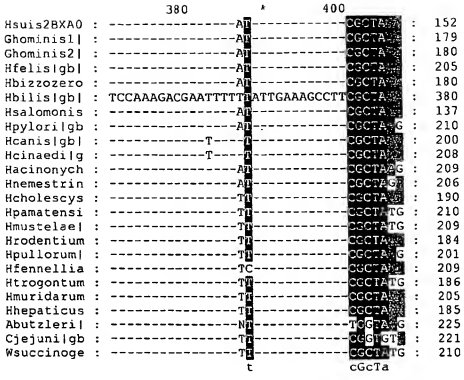

380
400
Hsuis2BXA0 : 152
Ghominis1| : 179
Ghominis2| : 180
Hfelis|gb| : 205
Hbizzozero : 180
Hbilis|gb| : TCCAAAGACGAATTTTTTATTGAAAGCCTT 380
Hsalomonis : 137
Hpylori|gb : 210
Hcanis|gb| : 200
Hcinaedi|g : 208
Hacinonych : 209
Hnemestrin : 206
Hcholescys : 190
Hpamatensi : 210
Hmustelae| : 209
Hrodentium : 184
Hpullorum| : 201
Hfennellia : 209
Htrogontum : 186
Hmuridarum : 205
Hhepaticus : 185
Abutzleri| : 225
Cjejuni|gb : 221
Wsuccinoge : 210

Figure 2 - 11

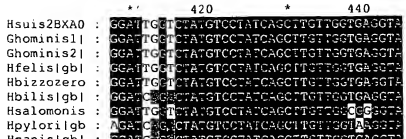

420
440
Hsuis2BXA0 : 189
Ghominis1| : 216
Ghominis2| : 217
Hfelis|gb| : 242
Hbizzozero : 217
Hbilis|gb| : 417
Hsalomonis : 174
Hpylori|gb : 247
Hcanis|gb| : 237
Hcinaedi|g : 245
Hacinonych : 246
Hnemestrin : 243
Hcholescys : 227
Hpamatensi : 247
Hmustelae| : 246
Hrodentium : 221
Hpullorum| : 238
Hfennellia : 246
Htrogontum : 223
Hmuridarum : 242
Hhepaticus : 222
Abutzleri| : 262
Cjejuni|gb : 258
Wsuccinoge : 247
gGAT G CTaTgtccTATCAGcTtGTTGGtgaGGTA

Figure 2 - 12

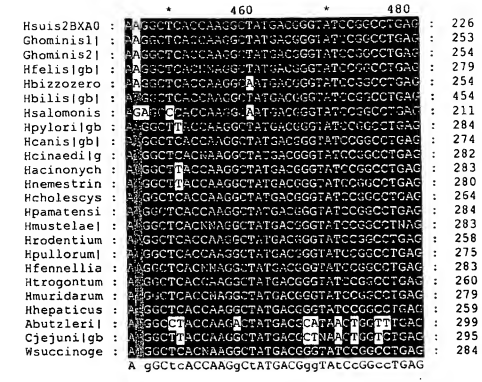

* 460 * 480
Hsuis2BXA0 : AAGGCTCACCAAGGCTATGACGGTATCCGCCCTGAG : 226
Ghominis1| : AAGGCTCACCAAGGCTATGACGGGTATCCGCCCTGAG : 253
Ghominis2| : AAGGCTCACCAAGGCTATGACGGGTATCCGGCCTGAG : 254
Hfelis|gb| : AAGGCTCACCAAGGCTATGACGGTATCCGGCCTGAG : 279
Hbizzozero : AAGGCTCACCAAGGCAATGACGGTATCCGGCCTGAG : 254
Hbilis|gb| : AAGGCTCACCAAGGCTATGACGGTATCCGCCCTGAG : 454
Hsalomonis : AGATGCCACCAATGCAATGACGGTATCCGCCTGAG : 211
Hpylori|gb : AAGGCTTACCAAGGCTATGACGGTATCCGCCTGAG : 284
Hcanis|gb| : AAGGCTCACCAAGGCTATGACGGTATCGGCCTGAG : 274
Hcinaedi|g : AAGGCTCACNAAGGCTATGACGGGTATCCGGCCTGAG : 282
Hacinonych : AAGGCTTACCAAGGCTATGACGGGTATCCGGCCTGAG : 283
Hnemestrin : AAGGCTTACCAAGGCTATGACGGGTATCCGGCCTGAG : 280
Hcholescys : AAGGCTCACCAAGGCTATGACGGGTATCCGGCCTGAG : 264
Hpamatensi : AAGGCTCACCAAGGCTATGACGGGTATCCGGCCTGAG : 284
Hmustelae| : AAGGCTCACNNAGGCTATGACGGGTATCCGGCCTNAG : 283
Hrodentium : AAGGCTCACCAAGGCTATGACGGGTATCCGGCCTGAG : 258
Hpullorum| : AAGGCTCACCAAGGCTATGACGGGTATCCGGCCTGAG : 275
Hfennellia : AAGGCTCACNNAGGCTATGACGGGTATCCGGCCTGAG : 283
Htrogontum : AAGGCTCACCAAGGCTATGACGGGTATCCGGCCTGAG : 260
Hmuridarum : AAGGCTCACCNAGGCTATGACGGGTATCCGGCCTGAG : 279
Hhepaticus : AAGGCTCACCAAGGCTATGACGGGTATCCGGCCTGAG : 259
Abutzleri| : AAGGCCTACCAAGACTATGACGCATAACTGGTTTGAC : 299
Cjejuni|gb : AAGGCTTACCAAGGCTATGACGCTNAACTGGTTGAC : 295
Wsuccinoge : AAGGCTCACNAAGGCTATGACGGGTATCCGGCCTGAG : 284
A gGCtcACCAAGgCtATGACGggTAtCCGGCcTGAG

Figure 2 - 13

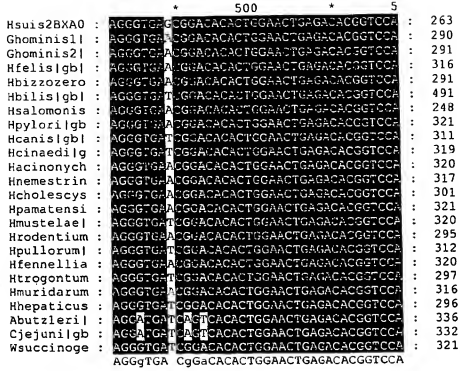

* 500 * 5
Hsuis2BXA0 : ACGGTGA CGGACACACTGGAACTGAGACACGGTCCA : 263
Ghominis1| : AGGGTGA CGGACACACTGGAACTGAGACACGGTCCA : 290
Ghominis2| : AGGGTGA CGGACACACTGGAACTGAGACACGGTCCA : 291
Hfelis|gb| : ACGGTGA CGGACACACTGGAACTGAGACACGGTCCA : 316
Hbizzozero : ACGGTGA CGGACACACTGGAACTGAGACACGGTCCA : 291
Hbilis|gb| : AGGGTGA CGGACACACTGGAACTGAGACACGGTCCA : 491
Hsalomonis : ACGGTGA CGGACACACTGGAACTGAGACACGGTCCA : 248
Hpylori|gb : AGGGTGA CGGACACACTGGAACTGAGACACGGTCCA : 321
Hcanis|gb| : AGGGTGA CGGACACACTCCAACTGAGACACGGTCCA : 311
Hcinaedi|g : AGGGTGA CGGACACACTGGAACTGAGACACGGTCCA : 319
Hacinonych : AGGGTGA CGGACACACTGGAACTGAGACACGGTCCA : 320
Hnemestrin : AGGGTGA CGGACACACTGGAACTGAGACACGGTCCA : 317
Hcholescys : AGGGTGA CGGACACACTGGAACTGAGACACGGTCCA : 301
Hpamatensi : AGGGTGA CGGACACACTGGAACTGAGACACGGTCCA : 321
Hmustelae| : AGGGTGA CGGACACACTGGAACTGAGACACGGTCCA : 320
Hrodentium : AGGGTGA CGGACACACTGGAACTGAGACACGGTCCA : 295
Hpullorum| : AGGGTGA CGGACACACTGGAACTGAGACACGGTCCA : 312
Hfennellia : AGGGTGA CGGACACACTGGAACTGAGACACGGTCCA : 320
Htrogontum : AGGGTGA CGGACACACTGGAACTGAGACACGGTCCA : 297
Hmuridarum : AGGGTGA CGGACACACTGGAACTGAGACACGGTCCA : 316
Hhepaticus : AGGGTGA CGGACACACTGGAACTGAGACACGGTCCA : 296
Abutzleri| : AGGATGA CGGTCACACTGGAACTGAGACACGGTCCA : 336
Cjejuni|gb : AGGATGA CGGTCACACTGGAACTGAGACACGGTCCA : 332
Wsuccinoge : AGGGTGA CGGACACACTGGAACTGAGACACGGTCCA : 321
AGGgTGA CgGaCACACTGGAACTGAGACACGGTCCA

Figure 2 - 14

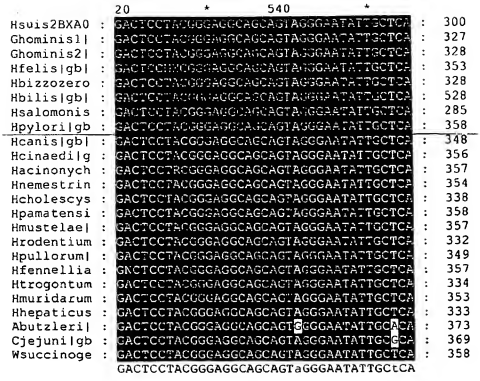

20 * 540 *
Hsuis2BXA0 : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 300
Ghominis1| : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 327
Ghominis2| : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 328
Hfelis|gb| : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 353
Hbizzozero : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 328
Hbilis|gb| : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 528
Hsalomonis : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 285
Hpylori|gb : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 358
Hcanis|gb| : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 348
Hcinaedi|g : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 356
Hacinonych : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 357
Hnemestrin : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 354
Hcholescys : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 338
Hpamatensi : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 358
Hmustelae| : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 357
Hrodentium : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 332
Hpullorum| : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 349
Hfennellia : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 357
Htrogontum : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 334
Hmuridarum : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 353
Hhepaticus : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 333
Abutzleri| : GACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACA : 373
Cjejuni|gb : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCGCA : 369
Wsuccinoge : GACTCCTACGGGAGGCAGCAGTAGGGAATATTGCTCA : 358
GACTCCTACGGGAGGCAGCAGTaGGGAATATTGCtCA

Figure 2 - 15

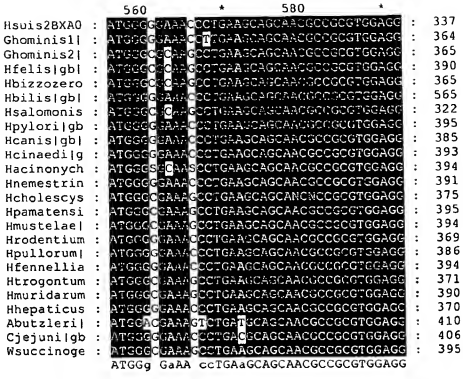

560
580
Hsuis2BXA0 : ATGGGGGAAACCCTGAAGCAGCAACGCCGCGTGGAGG : 337
Ghominis1| : ATGGGGGAAACCTTGGAACAGCAACGCCGCGTGGAGG : 364
Ghominis2| : ATGGGGGAAGCCTGAAGCAACGCCGCGTGGAGG : 365
Hfelis|gb| : ATGGGGGAAACCTGAAGCAGCAACGCCGCGTGGAGG : 390
Hbizzozero : ATGGGGGAAACCTGAAGCAGCAACGCCGCGTGGAGG : 365
Hbilis|gb| : ATGGGGGAAACCTGAAGCAGCAACGCCGCGTGGAGG : 565
Hsalomonis : ATGGGGGAAACCTGAAGCAGCAACGCCGCGTGGAGC : 322
Hpylori|gb : ATGGGGGAAACCTGAAGCAGCAACGCCGCGTGGAGC : 395
Hcanis|gb| : ATGGGGGAAACCTGAAGCAGCAACGCCGCGTGGAGG : 385
Hcinaedi|g : ATGGGGGAAACCTGAAGCAGCAACGCCGCGTGGAGG : 393
Hacinonych : ATGGGGGAAACCTGAAGCAGCAACGCCGCGTGGAGG : 394
Hnemestrin : ATGGGGGAAACCTGAAGCAGCAACGCCGCGTGGAGG : 391
Hcholescys : ATGGGGGAAACCTGAAGCAGCAACNCCGCGTGGAGG : 375
Hpamatensi : ATGGGGGAAACCTGAAGCAGCAACGCCGCGTGGAGG : 395
Hmustelae| : ATGGGGGAAACCTGAAGCAGCAACGCCGCGTGGAGG : 394
Hrodentium : ATGGGGGAAACCTGAAGCAGCAACGCCGCGTGGAGG : 369
Hpullorum| : ATGGGGGAAACCTGAAGCAGCAACGCCGCGTGGAGG : 386
Hfennellia : ATGGGGGAAACCTGAAGCAGCAACGCCGCGTGGAGG : 394
Htrogontum : ATGGGGGAAACCTGAAGCAGCAACGCCGCGTGGAGG : 371
Hmuridarum : ATGGGGGAAACCTGAAGCAGCAACGCCGCGTGGACC : 390
Hhepaticus : ATGGGGGAAACCTGAAGCAGCAACGCCGCGTGGAGC : 370
Abutzleri| : ATGGAGGAAAGTCTGATCAGCAACGCCGCGTGGAGG : 410
Cjejuni|gb : ATGGGGGAAACCTGAGCAGCAACGCCGCGTGGAGG : 406
Wsuccinoge : ATGGGGGAAAGCCTGAAGCAGCAACGCCGCGTGGAGG : 395
ATGGg GaAA ccTGAaGCAGCAACGCCGCGTGGAGG

Figure 2 – 16


600
*
620
Hsuis2BXA0 : ATGAAGGTTTTAGGATGGTAAACTCCTTTTGTTAGAG : 374
Ghominis1| : ATGAAGGTTTTAGGATTGTAAACTCCTTTTGTTAGAG : 401
Ghominis2| : ATGAAGGTTTTAGGATTGTAAACTCCTTTTGTTAGAG : 402
Hfelis|gb| : ATGAAGGTTTTAGGATTGTAAACTCCTTTTGTTAGAG : 427
Hbizzozero : ATGAAGGTTTTAGGATTGTAAACTCCTTTTGTTAGAG : 402
Hbilis|gb| : ATGAAGGTTTTAGGATTGTAAACTCCTTTTGTTAGAG : 602
Hsalomonis : ATGAAGGTTTTAGGATTGTAAACTCCTTTTGTTAGAG : 359
Hpylori|gb : ATGAAGGTTTTAGGATTGTAAACTCCTTTTGTTAGAG : 432
Hcanis|gb| : ATGAAGGTTTTAGGATTGTAAACTCCTTTTGTTAGAG : 422
Hcinaedi|g : ATGAAGGTTTTAGGATTGTAAACTCCTTTTGTTAGAG : 430
Hacinonych : ATGAAGGTTTTAGGATTGTAAACTCCTTTTGTCAGAG : 431
Hnemestrin : ATGAAGGTTTTAGGATTGTAAACTCCTTTTGTCAGAG : 428
Hcholescys : ATGAAGGTTTTAGGATTGTAAACTCCTTTTGTCAGAG : 412
Hpamatensi : ATGAAGGTTTTAGGATTGTAAACTCCTTTTGTTAGAG : 432
Hmustelae| : ATGAAGGTTTTAGGATTGTAAACTCCTTTTGTTAGAG : 431
Hrodentium : ATGAAGGTTTCGGATTGTAAACTCCTTTTGTTAGAG : 406
Hpullorum| : ATGAAGGTTTTCGGATTGTAAACTCCTTTTGTTAGAC : 423
Hfennellia : ATGAAGGTTTTAGGATTGTAAACTCCNNTTGTTAGAG : 431
Htrogontum : ATGAAGGTTTTAGGATTGTAAACTCCTTTTGTAAGAG : 408
Hmuridarum : ATGAAGGTTTTAGGATTGTAAACTCCTTTTGTGAGAG : 427
Hhepaticus : ATGAAGGTTTTAGGATTGTAAACTCCTTTTGTTAGAG : 407
Abutzleri| : ATGACACATTTCGGTGCGTAAACTCCTTTTGTATAAG : 447
Cjejuni|gb : ATGACACTTTTCGGAGCGTAAACTCCNNTCGTAGGC : 443
Wsuccinoge : ATGAAGGTCTTCGGATTGTAAACTCCTTTTCTAGAG : 432
ATGAaggttTTaGGattGTAAACTCCTTTT T agaG

Figure 2 - 17

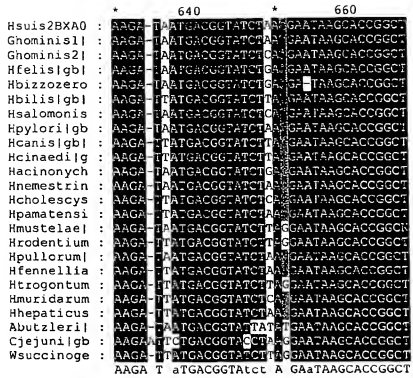
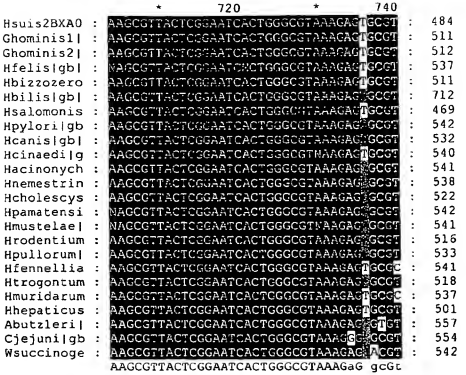

* 640 * 660
Hsuis2BXA0 : AAGA-TAATGACGGTATCTAATGGAATAAGCACCGGCT : 410
Ghominis1| : AAGA-TAATGACGGTATCTAATGGAATAAGCACCGGCT : 437
Ghominis2| : AAGA-TAATGACGGTATCTGATGAATAAGCACCGGCT : 438
Hfelis|gb| : AAGA-TAATGACGGTATCTGATGAATAAGCACCGGCT : 463
Hbizzozero : AAGA-TAATGACGGTATCTGATGG-TAAGCACCGGCT : 437
Hbilis|gb| : AAGA-TTATGACGGTATCTTATGATAAGCACCGGCT : 638
Hsalomonis : AAGA-TAATGACGGTATCTGATGAATAAGCACCGGCT : 395
Hpylori|gb : AAGA-TAATGACGGTATCTAATGAATAAGCACCGGCT : 468
Hcanis|gb| : AAGA-TTATGACGGTATCTTATGAATAAGCACCGGCT : 458
Hcinaedi|g : AAGA-TTATGACGGTATCTTATGAATAAGCACCGGCT : 466
Hacinonych : AAGA-TAATGACGGTATCTGATGAATAAGCACCGGCT : 467
Hnemestrin : AAGA-TAATGACGGTATCTAATGAATAAGCACCGGCT : 464
Hcholescys : AAGA-TTATGACGGTATCTGATGAATAAGCACCGGCT : 448
Hpamatensi : AAGA-TTATGACGGTATCTAATGAATAAGCACCGGCT : 468
Hmustelae| : AAGA-TAATGACGGTATCTTATGAATAAGCACCGGCN : 467
Hrodentium : AAGA-TTATGACGGTATCTTATGAATAAGCACCGGCT : 442
Hpullorum| : AAGA-TAATGACGGTATCTAATGAATAAGCACCGGCT : 459
Hfennellia : AAGA-TTATGACGGTATCTAATGAATAAGCACCGGCT : 467
Htrogontum : AAGA-TTATGACGGTATCTTATGAATAAGCACCGGCT : 444
Hmuridarum : AAGA-TTATGACGGTATCTGATGAATAAGCACCGGCT : 463
Hhepaticus : AAGA-TTATGACGGTATCTAATGAATAAGCACCGGCT : 443
Abutzleri| : AAGA-TAATGACGGTATATGATGAATAAGCACCGGCT : 483
Cjejuni|gb : AAGATTTCTGACGGTATCTATGGAATAAGCACCGGCT : 480
Wsuccinoge : AAGA-TTATGACGGTATCTTTGGAATAAGCACCGGCT : 468
AAGA T aTGACGGTAtct A GAaTAAGCACCGGCT

Figure 2 - 18


* 680 * 700
Hsuis2BXA0 : AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC : 447
Ghominis1| : AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC : 474
Ghominis2| : AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC : 475
Hfelis|gb| : AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC : 500
Hbizzozero : AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC : 474
Hbilis|gb| : AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC : 675
Hsalomonis : AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC : 432
Hpylori|gb : AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC : 505
Hcanis|gb| : AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC : 495
Hcinaedi|g : AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC : 503
Hacinonych : AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC : 504
Hnemestrin : AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC : 501
Hcholescys : AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC : 485
Hpamatensi : AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC : 505
Hmustelae| : AACTCCGTGCCAGCAGCCGCGGNAATACGGAGGGTGC : 504
Hrodentium : AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC : 479
Hpullorum| : AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC : 496
Hfennellia : AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC : 504
Htrogontum : AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC : 481
Hmuridarum : AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC : 500
Hhepaticus : AACTCCGTGCC---------- CGGAGGGTGC : 464
Abutzleri| : AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC : 520
Cjejuni|gb : AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC : 517
Wsuccinoge : AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC : 505
AACTCCGTGCCagcagccgcggtaataCGGAGGGTGC

Figure 2 - 19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Hsuis2BXA0 : AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCGT : 484
Ghominis1| : AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCGT : 511
Ghominis2| : AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCGT : 512
Hfelis|gb| : AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCGT : 537
Hbizzozero : AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCGT : 511
Hbilis|gb| : AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCGT : 712
Hsalomonis : AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCGT : 469
Hpylori|gb : AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCGT : 542
Hcanis|gb| : AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCGT : 532
Hcinaedi|g : AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCGT : 540
Hacinonych : AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCGT : 541
Hnemestrin : AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCGT : 538
Hcholescys : AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCGT : 522
Hpamatensi : NAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCGT : 542
Hmustelae| : NAGCGTTACTCGGAATCACTGGGCGTNAAGAGTGCGT : 541
Hrodentium : AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCGT : 516
Hpullorum| : AAGCGTTACTCGGAATCACTGGGCGTAAAGANTGCGT : 533
Hfennellia : AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCGC : 541
Htrogontum : AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCGT : 518
Hmuridarum : AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCGC : 537
Hhepaticus : AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCGT : 501
Abutzleri| : AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGTGT : 557
Cjejuni|gb : AAGCGTTACTCGGAATCACTGGGCGTAAAGGGTGCGT : 554
Wsuccinoge : AAGCGTTACTCGGAATCACTGGGCGTAAAGAACGT : 542
AAGCGTTACTCGGAATCACTGGGCGTAAAGaG gcGt

Figure 2 – 20

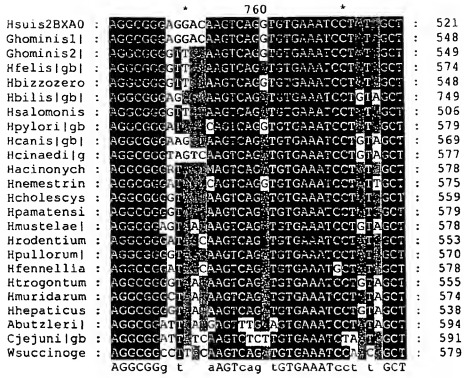
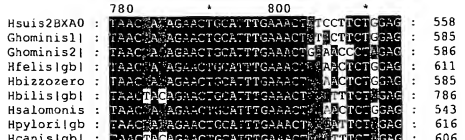

760
Hsuis2BXA0 : AGGCGGGAGGACAAGTCAGGTGTGAAATCCTATTGCT : 521
Ghominis1| : AGCCGGGAGGACAAGTCAGGTGTGAAATCCTATTGCT : 548
Ghominis2| : AGGCGGGTTGAAAGTCAGGTGTGAAATCCTATTGCT : 549
Hfelis|gb| : AGGCGGGTTGAAAGTCAGGTGTGAAATCCTATTGCT : 574
Hbizzozero : AGGCGGGTTGAAAGTCAGGTGTGAAATCCTATTGCT : 548
Hbilis|gb| : AGGCGGGAGGAAAGTCAGGTGTGAAATCCTGTAGCT : 749
Hsalomonis : AGGCGGGCGTTAAAGTCAGGTGTGAAATCCTATTGCT : 506
Hpylori|gb : AGGCGGGTTGAAGCAGTCAGGTGTGAAATCCTATTGCT : 579
Hcanis|gb| : AGGCGGGAAGAAAGTCAGGTGTGAAATCCTGTAGCT : 569
Hcinaedi|g : AGGCGGGTAGTCAAGTCAGGTGTGAAATCCTGTAGCT : 577
Hacinonych : AGCCGGCATGAAAGTCAGGTGTGAAATCCTATTGCT : 578
Hnemestrin : AGGCGGGTTGAAGCAGTCAGGTGTGAAATCCTATTGCT : 575
Hcholescys : AGGCGGGCGTAAAGTCAGGTGTGAAATCCTATTGCT : 559
Hpamatensi : AGCCGGGCGTAAAGTCAGGTGTGAAATCCTATTGCT : 579
Hmustelae| : AGGCGGGAGTAAAGTCAGGTGTGAAATCCTGTAGCT : 578
Hrodentium : AGGCGGGATAACAAGTCAGTTGTGAAATCCTATTGCT : 553
Hpullorum| : AGGCGGGCGTAAAGTCAGGTGTGAAATCCTATTGCT : 570
Hfennellia : AGGCCGGATAACAAGTCAGTTGTGAAATTGCTATTGCT : 578
Htrogontum : AGCCGGGCGTAAAGTCAGGTGTGAAATCCTGTAGCT : 555
Hmuridarum : AGGCGGGCTTAAAGTCAGGTGTGAAATCCTATTGCT : 574
Hhepaticus : AGGCGGGCGTAAAGTCAGGTGTGAAATCCTGTAGCT : 538
Abutzleri| : AGGCGGATTAAAGTTTGTAGTGAAATCCTATTGCT : 594
Cjejuni|gb : AGGCGGATTATCAGTCTTGTGAAATCTAATTGCT : 591
Wsuccinoge : AGCGGCCTTACAAGTCAGGTGTGAAATCCTACGCT : 579
AGGCGGg t aAGTcag tGTGAAATcct t GCT

Figure 2 -21


780
800
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Ghominis1| : 585
Ghominis2| : 586
Hfelis|gb| : 611
Hbizzozero : 585
Hbilis|gb| : 786
Hsalomonis : 543
Hpylori|gb : 616
Hcanis|gb| : 606
Hcinaedi|g : 614
Hacinonych : 615
Hnemestrin : 612
Hcholecys : 596
Hpamatensi : 616
Hmustelae| : 615
Hrodentium : 590
Hpullorum| : 607
Hfennellia : 615
Htrogontum : 592
Hmuridarum : 611
Hhepaticus : 575
Abutzleri| : 631
Cjejuni|gb : 628
Wsuccinoge : 616
TAAC a agAACTGCaTttgAAACT a tCT GAg

Figure 2 - 22

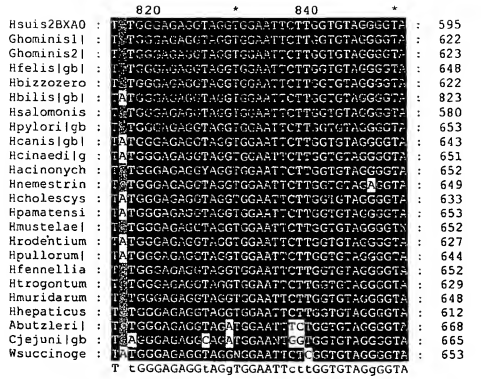
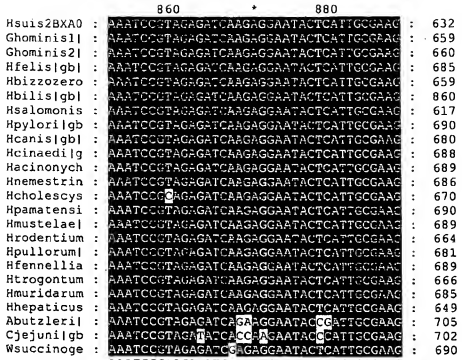

820 * 840 *
Hsuis2BXA0 : TGTGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA : 595
Ghominis1| : TGTGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA : 622
Ghominis2| : TGTGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA : 623
Hfelis|gb| : TGTGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA : 648
Hbizzozero : TGTGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA : 622
Hbilis|gb| : TATGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA : 823
Hsalomonis : TGTGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA : 580
Hpylori|gb : TGTGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA : 653
Hcanis|gb| : TATGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA : 643
Hcinaedi|g : TATGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA : 651
Hacinonych : TGTGGGAGAGGYAGGTGGAATTCTTGGTGTAGGGGTA : 652
Hnemestrin : TGTGGGAGAGGTAGGTGGAATTCTTGGTGTAGAGGTA : 649
Hcholescys : TATGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA : 633
Hpamatensi : TATGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA : 653
Hmustelae| : TGTGGGAGAGCTACGTGGAATTCTTGGTGTAGGGGTN : 652
Hrodentium : TATGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA : 627
Hpullorum| : TATGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA : 644
Hfennellia : TGTGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA : 652
Htrogontum : TGTGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA : 629
Hmuridarum : TGTGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA : 648
Hhepaticus : TGTGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA : 612
Abutzleri| : TGTGGGAGAGGTAGATGGAATTTCTGGTGTACGGGTA : 668
Cjejuni|gb : TGAGGGAGAGGCAGATGGAANTGGTGGTGTAGCGGTA : 665
Wsuccinoge : TATGGGAGAGGTAGGNGGAATTCTCGGTGTAGGGGTA : 653
T tGGGAGAGGtAGgTGGAATTcttGGTGTAGgGGTA

Figure 2 - 23


860
880
Hsuis2BXA0 : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 632
Ghominis1| : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 659
Ghominis2| : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 660
Hfelis|gb| : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 685
Hbizzozero : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 659
Hbilis|gb| : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 860
Hsalomonis : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 617
Hpylori|gb : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 690
Hcanis|gb| : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 680
Hcinaedi|g : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 688
Hacinonych : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 689
Hnemestrin : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 686
Hcholescys : AAATCCGCAGAGATCAAGAGGAATACTCATTGCGAAG : 670
Hpamatensi : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 690
Hmustelae| : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 689
Hrodentium : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 664
Hpullorum| : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 681
Hfennellia : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 689
Htrogontum : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 666
Hmuridarum : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 685
Hhepaticus : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 649
Abutzleri| : AAATCCGTAGACATCAGAGGAATACCGCATTGCGAAG : 705
Cjejuni|gb : AAATCCGTAGATTACCACCGAGAATACCCATTGCGAAG : 702
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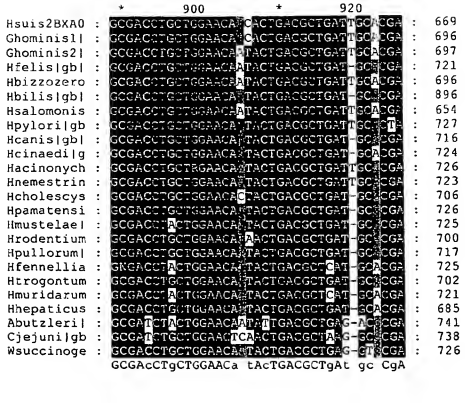
AAATCCGtAGAgATCaagAgGAATACtcATTGCGAAG

Figure 2 - 24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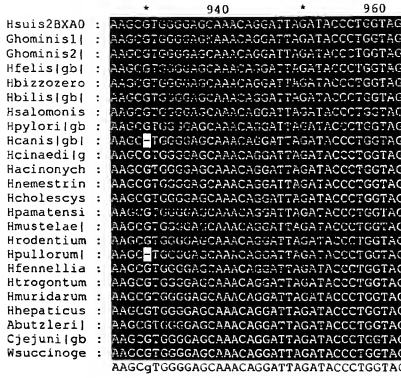
Hsuis2BXA0 : GCGACCTGCTGGAACACACTGACGCTGATTGCACGA : 669
Ghominis1| : GCGACCTGCTGGAACACACTGACGCTGATTGCACGA : 696
Ghominis2| : GCGACCTGCTGGAACACACTGACGCTGATTGCACGA : 697
Hfelis|gb| : GCGACCTGCTGGAACACACTGACGCTGATTGCACGA : 721
Hbizzozero : GCGACCTGCTGGAACACACTGACGCTGATTGCACGA : 696
Hbilis|gb| : GCGACCTGCTGGAACACACTGACGCTGATTGCACGA : 896
Hsalomonis : GCGACCTGCTGGAACACACTGACGCTGATTGCACGA : 654
Hpylori|gb : GCGACCTGCTGGAACACACTGACGCTGATTGCACGA : 727
Hcanis|gb| : GCGACCTGCTGGAACACACTGACGCTGATTGCACGA : 716
Hcinaedi|g : GCGACCTGCTGGAACACACTGACGCTGATTGCACGA : 724
Hacinonych : GCGACCTGCTGGAACACACTGACGCTGATTGCACGA : 726
Hnemestrin : GCGACCTGCTGGAACACACTGACGCTGATTGCACGA : 723
Hcholescys : GCGACCTGCTGGAACACACTGACGCTGATTGCACGA : 706
Hpamatensi : GCGACCTGCTGGAACACACTGACGCTGATTGCACGA : 726
Hmustelae| : GCGACCTACTGGAACACACTGACGCTGATTGCACGA : 725
Hrodentium : GCGACCTGCTGGAACACACTGACGCTGATTGCACGA : 700
Hpullorum| : GCGACCTGCTGGAACACACTGACGCTGATTGCACGA : 717
Hfennellia : GCGACCTACTGGAACACACTGACGCTGATTGCACGA : 725
Htrogontum : GCGACCTGCTGGAACACACTGACGCTGATTGCACGA : 702
Hmuridarum : GCGACCTACTGGAACACACTGACGCTGATTGCACGA : 721
Hhepaticus : GCGACCTGCTGGAACACACTGACGCTGATTGCACGA : 685
Abutzleri| : GCGATCTACTGGAACACACTGTGCCTGACGCACGA : 741
Cjejuni|gb : GCGATCTGCTGGAACTCACTGACGCTAGCGCGA : 738
Wsuccinoge : GCGACCTGCTGGAACACACTGACGCTGAGCGTCGA : 726
GCGAcCTgCTGGAACa tACTGACGCTgAt gc CgA

Figure 2 - 25


* 940 * 960
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Ghominis1| : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 733
Ghominis2| : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 734
Hfelis|gb| : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 758
Hbizzozero : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 733
Hbilis|gb| : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 933
Hsalomonis : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 691
Hpylori|gb : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 764
Hcanis|gb| : AAGC-TGGGGAGCAAACAGGATTAGATACCCTGGTAG : 752
Hcinaedi|g : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 761
Hacinonych : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 763
Hnemestrin : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 760
Hcholescys : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 743
Hpamatensi : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 763
Hmustelae| : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 762
Hrodentium : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 737
Hpullorum| : AAGC-TGCGGAGCAAACAGGATTAGATACCCTGGTAG : 753
Hfennellia : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 762
Htrogontum : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 739
Hmuridarum : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 758
Hhepaticus : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAC : 722
Abutzleri| : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 778
Cjejuni|gb : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 775
Wsuccinoge : AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG : 763
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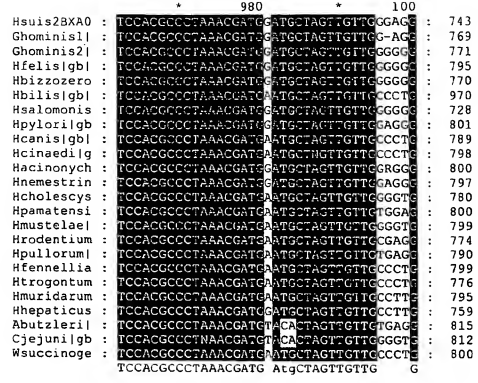
Figure 2 - 26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Ghominisl| : TCCACGCCCTAAACGATGGATGCTAGTTGTTGG-AGG : 769
Ghominis2| : TCCACGCCCTAAACGATGGATGCTAGTTGTTGGGGG : 771
Hfelis|gb| : TCCACGCCCTAAACGATGGATGCTAGTTGTTGGGGG : 795
Hbizzozero : TCCACGCCCTAAACGATGGATGCTAGTTGTTGGGGG : 770
Hbilis|gb| : TCCACGCCCTAAACGATCAATGCTAGTTGTTGCCCT : 970
Hsalomonis : TCCACGCCCTAAACGATGGATGCTAGTTGTTGGGGG : 728
Hpylori|gb : TCCACGCCCTAAACGATGGATGCTAGTTGTTGGAGG : 801
Hcanis|gb| : TCCACGCCCTAAACGATGAATGCTAGTTGTTGCCCT : 789
Hcinaedi|g : TCCACGCCCTAAACGATGAATGCTAGTTGTTGCCCT : 798
Hacinonych : TCCACGCCCTAAACGATGGATGCTAGTTGTTGGRGG : 800
Hnemestrin : TCCACGCCCTAAACGATGGATGCTAGTTGTTGGAGG : 797
Hcholescys : TCCACGCCCTAAACGATGAATGCTAGTTGTTGGGGT : 780
Hpamatensi : TCCACGCCCTAAACGATGAATGCTAGTTGTTGTGGA : 800
Hmustelae| : TCCACGCCCTAAACGATGAATGCTAGTTGTTGGGGT : 799
Hrodentium : TCCACGCCCTAAACGATGAATGCTAGTTGTTGCGAG : 774
Hpullorum| : TCCACGCCCTAAACGATGAATGCTAGTTGTTGTGAG : 790
Hfennellia : TCCACGCCCTAAACGATGAATGCTAGTTGTTGCCCT : 799
Htrogontum : TCCACGCCCTAAACGATGAATGCTAGTTGTTGCCCT : 776
Hmuridarum : TCCACGCCCTAAACGATGAATGCTAGTTGTTGCCTT : 795
Hhepaticus : TCCACGCCCTAAACGATGGATGCTAGTTGTTGCCTT : 759
Abutzleri| : TCCACGCCCTAAACGATGTACAGTAGTTGTTGTGAG : 815
Cjejuni|gb : TCCACGCCCTNAACGATGTACAGTAGTTGTTGGGGT : 812
Wsuccinoge : TCCACGCCCTAAACGATGAATGCTAGTTGTTGCCCT : 800
TCCACGCCCTAAACGATG AtgCTAGTTGTTG G

Figure 2 - 27


0
*
1020
*
Hsuis2BXA0 : CTTTGTGTTTCCAGTAATGCAGCTAACGCGTAAGCA : 780
Ghominis1| : CTTTGTGTTTCCAGTAATGCGCGTAACGCGTTAANNA : 806
Ghominis2| : CTTTGTGCTCCCAGTAATGCAGCTAACGCGTTAAGCA : 808
Hfelis|gb| : CTT-GTGCTCCCAGTAATGCAGCTAACGCGTTAAGCA : 831
Hbizzozero : CTTTGTGCCCCCAGTAATGCAGCTAACGCGTTAAGCA : 807
Hbilis|gb| : CTT-GTGAGGGCAGTAATGCAGCTAACGCGTTAAGCA : 1006
Hsalomonis : CTTTGTGCCCCCAGTAATGCAGCTAACGWCGTTAAGCA : 765
Hpylori|gb : CTTAGTGTCTCCAGTAATGCAGCTAACGCGTTAAGCA : 838
Hcanis|gb| : CTT-GTCAGGGCAGTAATGCAGCTAACGCGTTAAGCA : 825
Hcinaedi|g : CTT-NTCAGGGCAGTAATGCAGCTAACGCGTTAAGCA : 834
Hacinonych : CTTTGTGYYYCCAGTAATGCAGCTAACGCGTTAAGCA : 837
Hnemestrin : CTTAGTGTCTCCAGTAATGCACGTAACGCGTTAAGCA : 834
Hcholescys : CTT-GTGACTCCAGTAATGCAGCTAACGCGTTAAGCA : 816
Hpamatensi : CTT-GTGTCTGCAGTAATGCAGCTAACGCGTTAAGCA : 836
Hmustelae| : CTT-GTCACTCCAGTAATGCAGTTAACGCGTTAAGCA : 835
Hrodentium : CTT-GTGCTTGCAGTAATGCAGCTAACGCGTTAAGCA : 810
Hpullorum| : CTT-GTGCTTGCAGTAATGCAGCTAACGCGTTAAGCA : 826
Hfennellia : CTC-GTGAGGGCAGTAATGCAGCTAACGCGTTAAGCA : 835
Htrogontum : CTT-GTGAGGGCAGTAATGCAGCTAACGCGTTAAGCA : 812
Hmuridarum : CTT-GTGAGGGCAGTAATGCAGCTAACGCGTTAAGCA : 831
Hhepaticus : CTT-GTGAGGGCAGTAATGCAGCTAACGCGTTAAGCA : 795
Abutzleri| : CTC-GAGCTTGCAGTAATGCAGTTAACGCGTTAAGTG : 851
Cjejuni|gb : CTA-GCCATCTCAGTAATGCAGCTAACGCGTTAAGTG : 848
Wsuccinoge : CTT-GTGAGGGCAGTAATGCAGTTAACGCGTTAAGCA : 836
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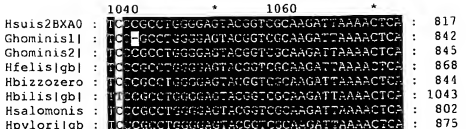
Figure 2 - 28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Ghominis2| : TCCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 845
Hfelis|gb| : TCCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 868
Hbizzozero : TCCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 844
Hbilis|gb| : TCCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 1043
Hsalomonis : TCCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 802
Hpylori|gb : TCCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 875
Hcanis|gb| : TCCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 862
Hcinaedi|g : TCCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 871
Hacinonych : TCCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 874
Hnemestrin : TCCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 871
Hcholescys : TCCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 853
Hpamatensi : TCCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 873
Hmustelae| : TCCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 872
Hrodentium : TCCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 847
Hpullorum| : TCCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 863
Hfennellia : TCCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 872
Htrogontum : TCCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 849
Hmuridarum : TCCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 868
Hhepaticus : TCCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 832
Abutzleri| : TACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 888
Cjejuni|gb : TACCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 885
Wsuccinoge : TCCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA : 873
T CcGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA

Figure 2 - 29

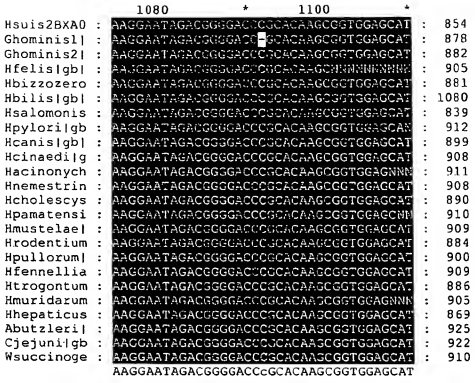
1080 * 1100 *
Hsuis2BXA0 : AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT : 854
Ghominis1| : AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT : 878
Ghominis2| : AAGGAATAGACGGGGACCGCACAAGCGGTGGAGCAT : 882
Hfelis|gb| : AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT : 905
Hbizzozero : AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT : 881
Hbilis|gb| : AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT : 1080
Hsalomonis : AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT : 839
Hpylori|gb : AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT : 912
Hcanis|gb| : AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT : 899
Hcinaedi|g : AAGGAATAGACGGGGACCCCCACAAGCGGTGGAGCAT : 908
Hacinonych : AAGGAATAGACGGGGACCCCCACAAGCGGTGGAGNNN : 911
Hnemestrin : AAGGAATAGACGGGGACCCCCACAAGCGGTGGACCAT : 908
Hcholescys : AAGGAATAGACGGGGACCCCGCACAAGCGGTGGAGCAT : 890
Hpamatensi : AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCNN : 910
Hmustelae| : AAGGAATAGACGCGGACCCGCACAAGCGGTGGACCAT : 909
Hrodentium : AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT : 884
Hpullorum| : AAGGAATAGACGGGGACCCGCACAAGCGGTGGACCAT : 900
Hfennellia : AAGGAATAGACGGGGACCCCCACAAGCGGTGGACCAT : 909
Htrogontum : AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT : 886
Hmuridarum : AAGGAATAGACGGGGACCCCGCACAAGCGGTGGAGNNN : 905
Hhepaticus : AAGGAATAGACGGGGACCCCGCACAAGCGGTGGAGCAT : 869
Abutzleri| : AAGGAATAGACGGGGACCCCGCACAAGCGGTGGAGCAT : 925
Cjejuni|gb : AAGGAATAGACGGGGACCCCGCACAAGCGGTGGAGCAT : 922
Wsuccinoge : AAGGAATAGACGGGGACCCCGCACAAGCGGTGGACCAT : 910
AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT

Figure 2 - 30


1120 * 1140
Hsuis2BXA0 : GTGGTTTAATTCGAAGTTACGCGAAGAACCTTACCTA : 891
Ghominis1| : GTGGTTTAATTCGAAGATAGAGCGAACGAACCTTACCTA : 915
Ghominis2| : GTGGTTTAATTCGAAGATAGAGCGAAGAACCTTACCTA : 919
Hfelis|gb| : GTGGTTTAATTCGAWNNNNNGCGAAGAACCTTACCTA : 942
Hbizzozero : GTGGTTTAATTCGAAGATAGACGAAGAACCTTACCTA : 918
Hbilis|gb| : GTGGTTTAATTCGAAGATAGCGAAGAACCTTACCTA : 1117
Hsalomonis : GTGGTTTAATTCGATTCGTAACGAAGAACCTTACCTA : 876
Hpylori|gb : GTGGTTTAATTCGANNNNNACGAAGAACCTTACCTA : 949
Hcanis|gb| : GTGGTTTAATTCGAAGATAGCGAAGAACCTTACCTA : 936
Hcinaedi|g : GTGGTTTAATTCGAGTATAGCGAAGAACCTTACCTA : 945
Hacinonych : GTGGTTTAATTCGANNNNNGAGAAGAACCTTACCTA : 948
Hnemestrin : GTGGTTTAATTCGAAGGTACAGAAGAACCTTACCTA : 945
Hcholescys : GTGGTTTAATTCGAAGATACGCGAAGAACCTTACCTA : 927
Hpamatensi : GTGGTTTAATTCGANNNTACGCGAAGAACCTTACCTA : 947
Hmustelae| : GTGGTTTAATTCGANNNTACGCGAAGAACCTTACCTA : 946
Hrodentium : GTGGTTTAATTCGAAGATAGACGAAGAACCTTACCTA : 921
Hpullorum| : GTGGTTTAATTCGAAGATAGCGCAAGAACCTTACCTA : 937
Hfennellia : GTGGTTTAATTCGANNTACGCGAAGAACCTTACCTA : 946
Htrogontum : GTGGTTTAATTCGAAGATACGCGAAGAACCTTACCTA : 923
Hmuridarum : GTGGTTTAATTCGANNNNACGCGAAGAACCTTACCTA : 942
Hhepaticus : GTGGTTTAATTCGAAGATACGCGAAGAACCTTACCTA : 906
Abutzleri| : GTGGTTTAATTCGANNNNACGAGAAGAACCTTACCTG : 962
Cjejuni|gb : GTGGTTTAATTCGAAGATACGCGAAGAACCTTACCTG : 959
Wsuccinoge : GTGGTTTAATTCGANNNNACGCGAAGAACCTTACCTG : 947
GTGGTTTAATTCGAagaTAC CGAAGAACCTTACCTa

Figure 2 -31

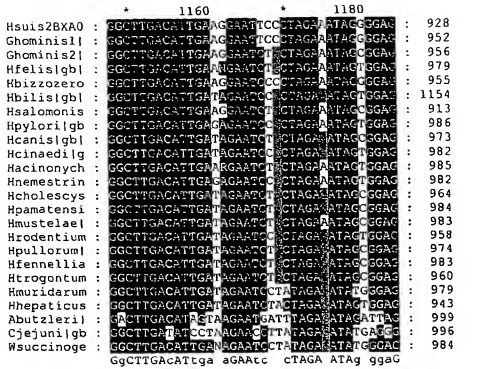
1160
1180
Hsuis2BXA0 : GGCTTGACATTGAAGGAATTCCCTAGAAATAGCGGAG : 928
Ghominis1| : GGCTTGACATTGAAGGAATTCCCTAGAAATAGCGGAG : 952
Ghominis2| : GGCTTGACATTGAAGGAATTCCCTAGAAATAGCGGAG : 956
Hfelis|gb| : GGCTTGACATTGAAGGAATTCCCTAGAAATAGCGGAG : 979
Hbizzozero : GGCTTGACATTGAAGGAATTCCCTAGAAATAGCGGAG : 955
Hbilis|gb| : GGCTTGACATTGATAGAATTCCCTAGAAATAGCGGAG : 1154
Hsalomonis : GGCTTGACATTGAAGGAATTCCCTAGAAATAGCGGAG : 913
Hpylori|gb : GGCTTGACATTGAAGAAATTCCCTAGAAATAGCGGAG : 986
Hcanis|gb| : GGCTTGACATTGATAGAATTCCCTAGAAATAGCGGAG : 973
Hcinaedi|g : GGCTTCACATTGATAGAATTCCCTAGAAATAGCGGAG : 982
Hacinonych : GGCTTGACATTGAAGAATTCCCTAGAAATAGCGGAG : 985
Hnemestrin : GGCTTGACATTGAAGAATTCCCTAGAAATAGCGGAG : 982
Hcholescys : GGCTTGACATTGATAGAATTCCCTAGAAATAGCGGAG : 964
Hpamatensi : GGCTTGACATTGATAGAATTCCCTAGAAATAGCGGAG : 984
Hmustelae| : GGCTTGACATTGATAGAATTCCCTAGAAATAGCGGAG : 983
Hrodentium : GGCTTGACATTGATAGAATTCCCTAGAAATAGCGGAG : 958
Hpullorum| : GGCTTGACATTGATAGAATTCCCTAGAAATAGCGGAG : 974
Hfennellia : GGCTTGACATTGATAGAATTCCCTAGAAATAGCGGAG : 983
Htrogontum : GGCTTGACATTGATAGAATTCCCTAGAAATAGCGGAG : 960
Hmuridarum : GGCTTGACATTGATAGAATTCCTAGAAATATTGGGAG : 979
Hhepaticus : GGCTTGACATTGATAGAATTCTACTAGAAATAGTGGAG : 943
Abutzleri| : GACTTGACATTGTAGAGATTGATTAGAGATAGATTAC : 999
Cjejuni|gb : GGCTTGATTCCTAAGAACGTTAAGAGATTGAGCG : 996
Wsuccinoge : GGCTTGACATTGANAGAATTCCTAGAAATATTGGAG : 984
GgCTTGAcATtga aGAAtc cTAGA ATAg ggaG

Figure 2 - 32

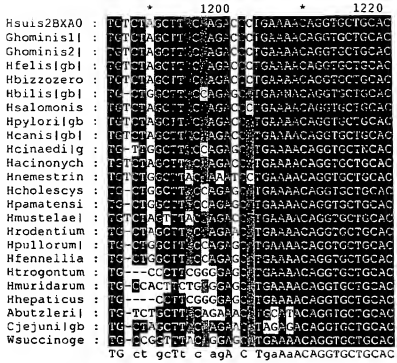
1200
1220
Hsuis2BXA0 : TGTCTGAGCTTACGAGACGACTGAAAACAGGTGCTGCAC : 965
Ghominis1| : TGTCTAAGCTTACGAGACGACTGAAAACAGGTGCTGCAC : 989
Ghominis2| : TGTCTAAGCTTACGAGACGACTGAAAACAGGTGCTGCAC : 993
Hfelis|gb| : TGTCTAAGCTTACGAGACGACTGAAAACAGGTGCTGCAC : 1016
Hbizzozero : TGTCTAAGCTTACGAGACGACTGAAAACAGGTGCTGCAC : 992
Hbilis|gb| : TG-CTGAGCTTACGAGACGACTGAANNACAGGTGCTGCAC : 1190
Hsalomonis : TGTCTAAGCTTACGAGACGACTGAAAACAGGTGCTGCAC : 950
Hpylori|gb : TGTCTAAGCTTACGAGACGACTGAAAACAGGTGCTGCAC : 1023
Hcanis|gb| : TGTCTAAGCTTACGAGACGACTGAAAACAGGTGCTGCAC : 1010
Hcinaedi|g : TG-CTGAGCTTACGAGACGACTGAAAACAGGTGCTKCAC : 1018
Hacinonych : TGTCTAAGCTTACGAGACGACTGAAAACAGGTGCTGCAC : 1022
Hnemestrin : TGTCTAAGCTTACGAATACTGAAAACAGGTGCTGCAC : 1019
Hcholescys : TG-CTGAGCTTACGAGACGACTGAAAACAGGTGCTGCAC : 1000
Hpamatensi : TG-CTGAGCTTACGAGACGACTGAAAACAGGTGCTGCAC : 1020
Hmustelae| : TGTCTAAGTTACGAGACGACTGAAAACAGGTGCTGCAC : 1020
Hrodentium : TG-CTAAGCTTACGAGACGACTGAAAACAGGTGCTGCAC : 994
Hpullorum| : TG-CTGAGCTTACGAGACGACTGAAAACAGGTGCTGCAC : 1010
Hfennellia : TG-CTGAGCTTACGAGACGACTGAAAACAGGTGCTGCAC : 1019
Htrogontum : TG---CCCTGCGGGGAGACGACTGAAAACAGGTGCTGCAC : 994
Hmuridarum : TG-GCACTTCTGGGGAGACGACTGAAAACAGGTGCTGCAC : 1015
Hhepaticus : TG----CCTTCGGGGAGACGACTGAAAACAGGTGCTGCAC : 976
Abutzleri| : TG-TCTGCTTACAGAAACGACTGAAACAGGTGCTGCAC : 1035
Cjejuni|gb : TG-CTAGCTTACGAGAACGACTAGAACACAGGTGCTGCAC : 1032
Wsuccinoge : TG-CCGCTTACGGGAGACGACTGAAAACAGGTGCTGCAC : 1020
TG ct gcTt c agA C TgaAaACAGGTGCTGCAC

Figure 2 - 33

```
                    *       1240            *       12
Hsuis2BXA0  : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1002
Ghominis1|  : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1026
Ghominis2|  : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTCGGTTAA : 1030
Hfelis|gb|  : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1053
Hbizzozero  : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1029
Hbilis|gb|  : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1227
Hsalomonis  : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA :  987
Hpylori|gb  : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1060
Hcanis|gb|  : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1047
Hcinaedi|g  : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1055
Hacinonych  : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTNA : 1059
Hnemestrin  : GGCTGTCGTCAGCTCGTGTCGTGACATGTTGGGTTAA : 1056
Hcholescys  : GGCTGTCGTCACCTCGTGTCGTCAGATGTTGGGTTAA : 1037
Hpamatensi  : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1057
Hmustelae|  : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1057
Hrodentium  : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1031
Hpullorum|  : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1047
Hfennellia  : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1056
Htrogontum  : GGCTGTCGTCAGCTCGTCTCGTGAGATGTTGGGTTAA : 1031
Hmuridarum  : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTNA : 1052
Hhepaticus  : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1013
Abutzleri|  : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1072
Cjejuni|gb  : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTNA : 1069
Wsuccinoge  : GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA : 1057
              GGCTGTCGTCAGCTCGTGTCGTGAgATGTTGGGTTAA
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Figure 2 - 34

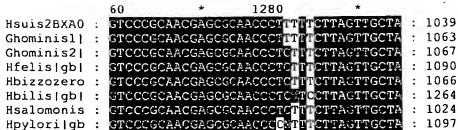

60 * 1280 *
Hsuis2BXA0 : GTCCCGCAACGAGCGCAACCCTTTTCTTAGTTGCTA : 1039
Ghominis1| : GTCCCGCAACGAGCGCAACCCTTTTCTTAGTTGCTA : 1063
Ghominis2| : GTCCCGCAACGAGCGCAACCCTCTTCTTAGTTGCTA : 1067
Hfelis|gb| : GTCCCGCAACGAGCGCAACCCTCTTCTTAGTTGCTA : 1090
Hbizzozero : GTCCCGCAACGAGCGCAACCCTCTTCTTAGTTGCTA : 1066
Hbilis|gb| : GTCCCGCAACGAGCGCAACCCTCTTCTTAGTTGCTA : 1264
Hsalomonis : GTCCCGCAACGAGCGCAACCCTCTTCTTAGTTGCTA : 1024
Hpylori|gb : GTCCCGCAACGAGCGCAACCCTCTTCTTAGTTGCTA : 1097
Hcanis|gb| : GTCCCGCAACGAGCGCAACCCTCTTCTTAGTTGCTA : 1084
Hcinaedi|g : GTCCCGCAACGAGCGCAACCCTCTTCTTAGTTGCTA : 1092
Hacinonych : GTCCCGCAACGAGCGCAACCCTCTTCTTAGTTGCTA : 1096
Hnemestrin : GTCCCGCAACGAGCGCAACCCTCTTCTTAGTTGCTA : 1093
Hcholecys : GTCCCGCAACGAGCGCAACCCTCTTCTTAGTTGCTA : 1074
Hpamatensi : GTCCCGCAACGAGCGCAACCCTCTTCTTAGTTGCTA : 1094
Hmustelae| : GTCCCGCAACGAGCGCAACCCTCTTCTTAGTTGCTA : 1094
Hrodentium : GTCCCGCAACGAGCGCAACCCTCTTCTTAGTCGCTA : 1068
Hpullorum| : GTCCCGCAACGAGCGCAACCCTCTTCTTAGTTGCTA : 1084
Hfennellia : GTCCCGCAACGAGCGCAACCCTCTTCTTAGTTGTTA : 1093
Htrogontum : GTCCCGCAACGAGCGCAACCCTCTTCTTAGTTGCTA : 1068
Hmuridarum : GTCCCGCAACGAGCGCAACCCTCTTCTTAGTTGCTA : 1089
Hhepaticus : N---------- : 1015
Abutzleri| : GTCCCGCAACGAGCGCAACCCTCTTCTTAGTTGCTA : 1109
Cjejuni|gb : GTCCCGCAACGAGCGCAACCCACTTATTAGTTGCTA : 1106
Wsuccinoge : GTCCCGCAACGAGCGCAACCCTCTTCACTAGTTGCTA : 1094
Gtcccgcaacgagcgcaaccctc t cttaGttgcta

Figure 2 - 35

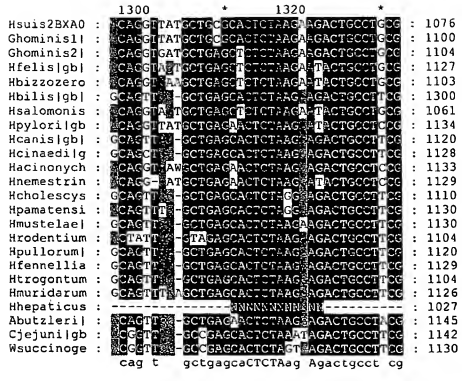

1300 * 1320 *
Hsuis2BXA0 : GCAGGTTATGCTGCGCATCTAAGTAGACTGCCTGG : 1076
Ghominis1| : GCAGGTTATGCTGCGCATCTAAGAAGACTGCCTGG : 1100
Ghominis2| : GCAGGTGATGCTGAGGTTTCTAAGAAGACTGCCTGC : 1104
Hfelis|gb| : GCAGGTAGTGCTGAGGTATCTAAGATTACTGCCTGG : 1127
Hbizzozero : GCAGGTAATGCTGAGGTATCTAAGATTACTGCCTGG : 1103
Hbilis|gb| : GCAGTTTG-GCTGAGCATTCTAAGAAGACTGCCTTG : 1300
Hsalomonis : GCAGGTAATGCTGAGGTATCTAAGATTACTGCCTGG : 1061
Hpylori|gb : GCAGGTTATGCTGACGAACTCTAAGATTACTGCCTGG : 1134
Hcanis|gb| : GCAGTTTG-GCTGAGCACTCTAAGAAGACTGCCTTG : 1120
Hcinaedi|g : GCAGCTTG-GCTGAGCACTTCTAAGAAGACTGCCTTG : 1128
Hacinonych : GCAGGTAAWGCTGAGGAACTCTAAGAAGACTGCCTGG : 1133
Hnemestrin : GCAGG-TATGCTGAGGAACTCTAAGAATACTGCCTGG : 1129
Hcholescys : GCAGTTTG-GCTGAGCACTCTTCGGAAGACTGCCTTG : 1110
Hpamatensi : GCAGTTTG-GCTGAGCACTCTTCGGAAGACTGCCTTG : 1130
Hmustelae| : GCAGTTTG-GCTGAGCACTCTTAAGAAGACTGCCTTG : 1130
Hrodentium : GCTATTTG-GTAGAGCACTCTTAAGAAGACTGCCTTG : 1104
Hpullorum| : GCAGTTTG-GCTGAGCACTCTAAGAAGACTGCCTTG : 1120
Hfennellia : GCAGTTTG-GCTGAGCACTCTTAAGAAGACTGCCTTG : 1129
Htrogontum : GCAGTTTG-GCTGAGCACTCTAAGAAGACTGCCTTG : 1104
Hmuridarum : GCAGTTTGAGCTGAGCACTCTAAGAAGACTGCCTTG : 1126
Hhepaticus : ----------GNNNNNNNNNN---------- : 1027
Abutzleri| : GCAGTTTG-GCTGAGCAGTCTAAGAAGACTGCCTTG : 1145
Cjejuni|gb : GCGTTTG-GCGAGCACTCTAAATAGACTGCCTTG : 1142
Wsuccinoge : GCGTTTG-GCGAGCACTCTATTTAGACTGCCTTG : 1130
cag t gctgagcaCTCTAag Agactgcct cg

Figure 2 - 36

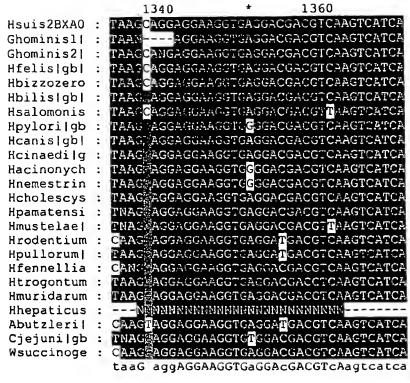
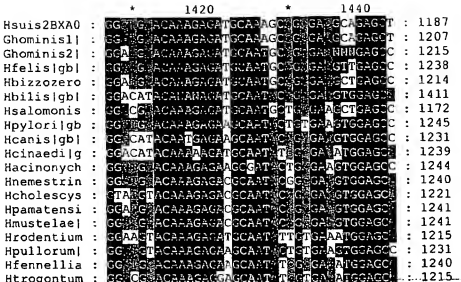

1340
*
1360
Hsuis2BXA0 : TAAGCAGGAGGAAGGTGAGGACGACGTCAAGTCATCA : 1113
Ghominis1| : TAAN----GGAAGGTGAGGACGACGTCAAGTCATCA : 1133
Ghominis2| : TAAGCANGAGGAAGGTGAGGACGACGTCAAGTCATCA : 1141
Hfelis|gb| : TAAGCAGGAGGAAGGTGAGGACGACGTCAAGTCATCA : 1164
Hbizzozero : TAAGCAGGAGGAAGGTGAGGACGACGTCAAGTCATCA : 1140
Hbilis|gb| : TAAGCAGGAGGAAGGTGAGGACGACGTCAAGTCATCA : 1337
Hsalomonis : TAAGCAGGAGGAAGGTGAGGACGACGTTAAGTCATCA : 1098
Hpylori|gb : TAAGCAGGAGGAAGGTGGGACGACGTCAAGTCATCA : 1171
Hcanis|gb| : TAAGCAGGACGAAGGTGAGGACGACGTCAAGTCATCA : 1157
Hcinaedi|g : TAAGCAGGAGGAAGGTGAGGACGACGTCAAGTCATCA : 1165
Hacinonych : TAAGCAGGAGGAAGGTGGGACGACGTCAAGTCATCA : 1170
Hnemestrin : TAAGCAGGAGGAAGGTGGGACGACGTCAAGTCATCA : 1166
Hcholescys : TAAGCAGGACGAAGGTGAGGACGACGTCAAGTCATCA : 1147
Hpamatensi : TNAGCAGGAGGAAGGTGAGGACGACGTCAAGTCATCA : 1167
Hmustelae| : TNAGCAGGAGGAAGGTGAGGACGACGTCAAGTCATCA : 1167
Hrodentium : CAAGCAGGAGGAAGGTGAGGACGACGTCAAGTCATCA : 1141
Hpullorum| : CAAGCAGGAGGAAGGTGAGGACGACGTCAAGTCATCA : 1157
Hfennellia : CANGCAGGAGGAAGGTGAGGACGACGTCAAGTCATCA : 1166
Htrogontum : TAAGCAGGAGGAAGGTGAGGACGACCTCAAGTCATCA : 1141
Hmuridarum : TAAGCAGGAGGAAGGTGAGGACGACGTCAAGTCATCA : 1163
Hhepaticus : ---NNNNNNNNNNNNNNNNNNNNNNNNNNN------- : 1053
Abutzleri| : CAAGCAGGAGGAAGGTGAGGACGACGTCAAGTCATCA : 1182
Cjejuni|gb : TNAGCAGGACGAAGGTGAGGACGACGTCAAGTCATCA : 1179
Wsuccinoge : CAAGCAGGAGGAAGGTGAGGACGACGTCAAGTCATCA : 1167
taaG aggAGGAAGGTGaGGAcGACGTcAagtcatca

Figure 2 - 37


* 1380 * 1400
Hsuis2BXA0 : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1150
Ghominis1| : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1170
Ghominis2| : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1178
Hfelis|gb| : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1201
Hbizzozero : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1177
Hbilis|gb| : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1374
Hsalomonis : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1135
Hpylori|gb : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1208
Hcanis|gb| : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1194
Hcinaedi|g : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1202
Hacinonych : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1207
Hnemestrin : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1203
Hcholescys : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1184
Hpamatensi : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1204
Hmustelae| : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1204
Hrodentium : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1178
Hpullorum| : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1194
Hfennellia : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1203
Htrogontum : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1178
Hmuridarum : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1200
Hhepaticus : --------N----------NNN : 1057
Abutzleri| : TGGCCCTTACGTGCAGGGCTACACACGTGCTACAATG : 1219
Cjejuni|gb : TGGCCCTTATGCCCAGGGCGACACACGTGCTACAATC : 1216
Wsuccinoge : TGGCCCTTACGCCYAGGGCTACACACGTGCTACAATG : 1204
tggcccttAcgcctagggctacacacgtgctacaATG

Figure 2 - 38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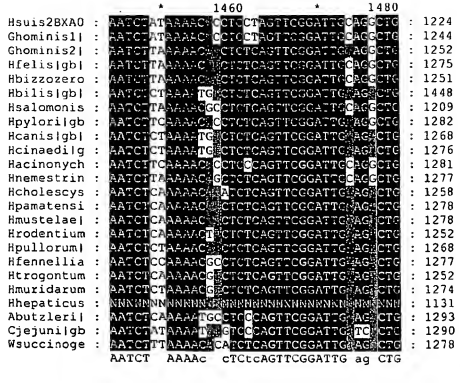
1440
Hsuis2BXA0 : 1187
Ghominis1| : 1207
Ghominis2| : 1215
Hfelis|gb| : 1238
Hbizzozero : 1214
Hbilis|gb| : 1411
Hsalomonis : 1172
Hpylori|gb : 1245
Hcanis|gb| : 1231
Hclnaedi|g : 1239
Hacinonych : 1244
Hnemestrin : 1240
Hcholescys : 1221
Hpamatensi : 1241
Hmustelae| : 1241
Hrodentium : 1215
Hpullorum| : 1231
Hfennellia : 1240
Htrogentum : 1215
Hmuridarum : 1237
Hhepaticus : 1094
Abutzleri| : 1256
Cjejuni|gb : 1253
Wsuccinoge : 1241
Gg g ACAAagAGa GCaAt c G GA gtgGAGC

Figure 2 - 39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1480
Hsuis2BXA0 : 1224
Ghominis1| : 1244
Ghominis2| : 1252
Hfelis|gb| : 1275
Hbizzozero : 1251
Hbilis|gb| : 1448
Hsalomonis : 1209
Hpylori|gb : 1282
Hcanis|gb| : 1268
Hcinaedi|g : 1276
Hacinonych : 1281
Hnemestrin : 1277
Hcholecys : 1258
Hpamatensi : 1278
Hmustelae| : 1278
Hrodentium : 1252
Hpullorum| : 1268
Hfennellia : 1277
Htrogontum : 1252
Hmuridarum : 1274
Hhepaticus : 1131
Abutzleri| : 1293
Cjejuni|gb : 1290
Wsuccinoge : 1278
AATCT AAAAc cTCtcAGTTCGGATTG ag CTG

Figure 2 -40


* 1500 * 1
Hsuis2BXA0 : 1261
Ghominisl| : 1281
Ghominis2| : 1289
Hfelis|gb| : 1312
Hbizzozero : 1288
Hbilis|gb| : 1485
Hsalomonis : 1246
Hpylori|gb : 1319
Hcanis|gb| : 1305
Hcinaedi|g : 1313
Hacinonych : 1318
Hnemestrin : 1314
Hcholescys : 1295
Hpamatensi : 1315
Hmustelae| : 1315
Hrodentium : 1289
Hpullorum| : 1305
Hfennellia : 1314
Htrogontum : 1289
Hmuridarum : 1311
Hhepaticus : 1168
Abutzleri| : 1330
Cjejuni|gb : 1327
Wsuccinoge : 1315
CAACTCG ct CATgAAGctGGAATCGCTAGTAATCG

Figure 2 - 41


520 * 1540 *
Hsuis2BXA0 : GAATCAGCTATGTAG CGGTGAATACGTTCCCGGGTC : 1298
Ghominis1| : GAATCAGCTATGTAG CGGTGAATACGTTCCCGGGTC : 1318
Ghominis2| : GAATCAGCTATGTAG CGGTGAATACGTTCCCGGGTC : 1326
Hfelis|gb| : GAATCAGCAATGTAG CGGTGAATACGTTCCCGGGTC : 1349
Hbizzozero : GAATCAGCAATGTAG CGGTGAATACGTTCCCGGGTC : 1325
Hbilis|gb| : TGAATCAGCAATGTCA CGGTGAATACGTTCCCGGGTC : 1522
Hsalomonis : GAATCAGCAATGTAG CGGTGAATACGTTCCCGGGTC : 1283
Hpylori|gb : GAATCAGCTATGTAG CGGTGAATACGTTCCCGGGTC : 1356
Hcanis|gb| : TGAATCAGCAATGTCA CGGTGAATACGTTCCCGGGTC : 1342
Hcinaedi|g : GAATCAGCAATGTAG CGGTGAATACGTTCCCGGGTC : 1350
Hacinonych : GAATCAGCAATGTAG CGGTGAATACGTTCCCGGGTC : 1355
Hnemestrin : TATCAGCAATGTAG CGGTGAATACGTTCCCGGGTC : 1351
Hcholescys : TGAATCAGCAATGTCA CGGTGAATACGTTCCCGGGTC : 1332
Hpamatensi : TGAATCAGCAATGTCA CGGTGAATACGTTCCCGGGTC : 1352
Hmustelae| : TGAATCAGCAATGTCA CGGTGAATACGTTCCCGGGTC : 1352
Hrodentium : TGATCAGCTATGCTA CGGTGAATACGTTCCCGGGTC : 1326
Hpullorum| : GAATCAGCAATGTAG CGGTGAATACGTTCCCGGGTC : 1342
Hfennellia : GAATCAGCAATGTAG CGGTGAATACGTTCCCGGGTC : 1351
Htrogontum : GAATCAGCAATGTAG CGGTGAATACGTTCCCGGGTC : 1326
Hmuridarum : TGAATCAGCAATGTCA CGGTGAATACGTTCCCGGGTC : 1348
Hhepaticus : NAATCAGCAATGTCA CGGTGAATACGTTCCCGGGTN : 1205
Abutzleri| : TGATCAGCTATGCTA CGGTGAATACGTTCCCGGGTC : 1367
Cjejuni|gb : TGATCAGCAATGCAA CGGTGAATACGTTCCCGGGTC : 1364
Wsuccinoge : TGATCAGCAATGCAA CGGTGAATACGTTCCCGGGTC : 1352
aATCAGC ATGt CGGTGAATACGTTCCCGGGTC

Figure 2 - 42

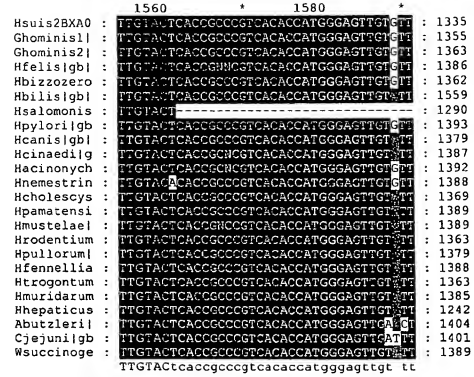

1560 * 1580 *
Hsuis2BXA0 : TTGTACTCACCGCCCGTCACACCATGGGAGTTGTCGTT : 1335
Ghominis1| : TTGTACTCACCGCCCGTCACACCATGGGAGTTGTCGTT : 1355
Ghominis2| : TTGTACTCACCGCCCGTCACACCATGGGAGTTGTCGTT : 1363
Hfelis|gb| : TTGTACTCACCGNMCGTCACACCATGGGAGTTGTCGTT : 1386
Hbizzozero : TTGTACTCACCGCCCGTCACACCATGGGAGTTGTCGTT : 1362
Hbilis|gb| : TTGTACTCACCGCCCGTCACACCATGGGAGTTGTCGTT : 1559
Hsalomonis : TTGTACT---------- : 1290
Hpylori|gb : TTGTACTCACCGCCCGTCACACCATGGGAGTTGTCGTT : 1393
Hcanis|gb| : TTGTACTCACCGCCCGTCACACCATGGGAGTTGTCGTT : 1379
Hcinaedi|g : TTGTACTCACCGCNCGTCACACCATGGGAGTTGTCGTT : 1387
Hacinonych : TTGTACTCACCGCNCGTCACACCATGGGAGTTGTCGTT : 1392
Hnemestrin : TTGTACACACCGCCCGTCACACCATGGGAGTTGTCGTT : 1388
Hcholescys : TTGTACTCACCGCCCGTCACACCATGGGAGTTGTCGTT : 1369
Hpamatensi : TTGTACTCACCGCCCGTCACACCATGGGAGTTGTCGTT : 1389
Hmustelae| : TTGTACTCACCGNCCGTCACACCATGGGAGTTGTCGTT : 1389
Hrodentium : TTGTACTCACCGCCCGTCACACCATGGGAGTTGTCGTT : 1363
Hpullorum| : TTGTACTCACCGCCCGTCACACCATGGGAGTTGTCGTT : 1379
Hfennellia : TTGTACTCACCGCCCGTCACACCATGGGAGTTGTCGTT : 1388
Htrogontum : TTGTACTCACCGCCCGTCACACCATGGGAGTTGTCGTT : 1363
Hmuridarum : TTGTACTCACCGCCCGTCACACCATGGGAGTTGTCGTT : 1385
Hhepaticus : TTGTACTCACCGCCCGTCACACCATGGGAGTTGTCGTT : 1242
Abutzleri| : TTGTACTCACCGCCCGTCACACCATGGGAGTTGACGT : 1404
Cjejuni|gb : TTGTACTCACCGCCCGTCACACCATGGGAGTTGCATTT : 1401
Wsuccinoge : TTGTACTCACCGCCCGTCACACCATGGGAGTTGTTTT : 1389
TTGTACtcaccgcccgtcacaccatgggagttgt tt

Figure 2 - 43

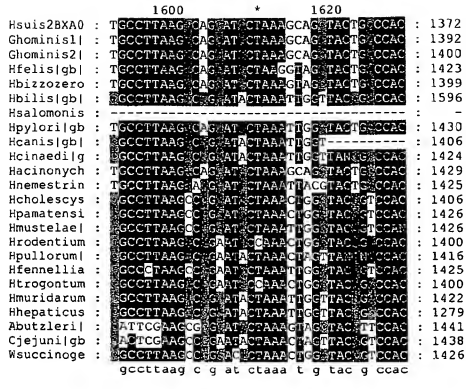

1600 * 1620
Hsuis2BXA0 : TGCCTTAAGCCAGGATGCTAAAGCAGGTACTGCCAC : 1372
Ghominisl| : TGCCTTAAGCCAGGATGCTAAAGCAGGTACTGCCAC : 1392
Ghominis2| : TGCCTTAAGCCAGGATGCTAAAGCAGGTACTGCCAC : 1400
Hfelis|gb| : TGCCTTAAGCCAGGATGCTAAGGTAGGTACTGCCAC : 1423
Hbizzozero : TGCCTTAAGCCAGGATGCTAAAGTAGGTACTGCCAC : 1399
Hbilis|gb| : TGCCTTAAGCCGGAATACTAAATTGGGTACTGCCAC : 1596
Hsalomonis : ---------- : -
Hpylori|gb : TGCCTTAAGCCAGGATGCTAAATTGGGTACTGCCAC : 1430
Hcanis|gb| : TGCCTTAAGCCGGAATACTAAATTGGT---------- : 1406
Hcinaedi|g : TGCCTTAAGCCGGAATACTAAATTGGTTANGGCCAC : 1424
Hacinonych : TGCCTTAAGCCAGGATGCTAAAGCAGGTACTGCCAC : 1429
Hnemestrin : TGCCTTAAGCAGGATGCTAAATTACGTACTGCCAC : 1425
Hcholescys : TGCCTTAAGCCGGATGCTAAACTGGGTACTGCCAC : 1406
Hpamatensi : TGCCTTAAGCCGGATGCTAAACTGGGTACTGCCAC : 1426
Hmustelae| : TGCCTTAAGCCGGATGCTAAATTGGGTACTGCCAN : 1426
Hrodentium : TGCCTTAAGCCGAATGCTAAACTGGGTACTGCCAC : 1400
Hpullorum| : TGCCTTAAGCCGAATACTAAACTAGTAATTGCCAC : 1416
Hfennellia : TGCCCTAAGCCGAATGCTAAATTGGGTACTGCCAC : 1425
Htrogontum : TGCCTTAAGCCGAATGCCAAACTGGGTACTGCCAC : 1400
Hmuridarum : TGCCTTAAGCCGAATACTAAATTGGTACTGCCAC : 1422
Hhepaticus : TGCCTTAAGCCGCATACTAATTGGTTACTGCCAC : 1279
Abutzleri| : TATTCGAAGCCGGATGCTAAAGTAGGTACTTCCAC : 1441
Cjejuni|gb : TATCTCGAAGCCGGAATACTAAACTAGTTACTGCCAC : 1438
Wsuccinoge : TGCCTTAAGCCGGATGCTAAACTGGGTACTGCCAC : 1426
gccttaag c g at ctaaa t g tac g ccac

Figure 2 - 44

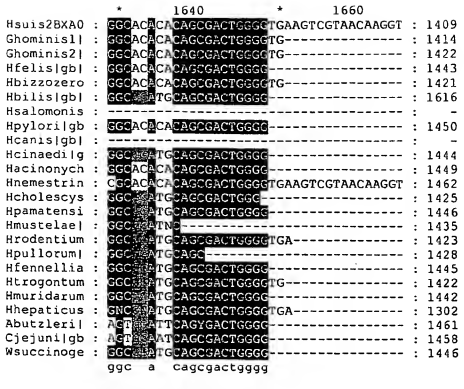
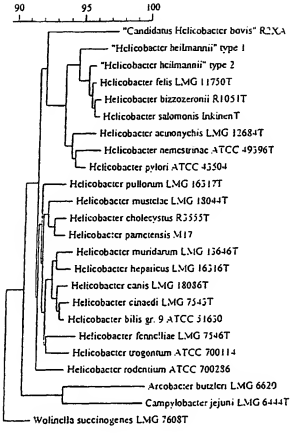

* 1640 * 1660
Hsuis2BXA0 : GGCACACACAGCGACTGGGGTGAAGTCGTAACAAGGT : 1409
Ghominis1| : GGCACACACAGCGACTGGGGTG---------- : 1414
Ghominis2| : GGCACACACAGCGACTGGGGTG---------- : 1422
Hfelis|gb| : GGCACACACAGCGACTGGGG---------- : 1443
Hbizzozero : GGCACACACAGCGACTGGGGTG---------- : 1421
Hbilis|gb| : GGCACATGCAGCGACTGGGG---------- : 1616
Hsalomonis : ---------- : -
Hpylori|gb : GGCACACACAGCGACTGGGG---------- : 1450
Hcanis|gb| : ---------- : -
Hcinaedi|g : GGCACATGCAGCGACTGGGG---------- : 1444
Hacinonych : GGCACACACAGCGACTGGGG---------- : 1449
Hnemestrin : CGCACACACAGCGACTGGGGTGAAGTCGTAACAAGGT : 1462
Hcholescys : GGCACATGCAGCGACTGGC---------- : 1425
Hpamatensi : GGCACATGCAGCGACTGGGG---------- : 1446
Hmustelae| : GGCACATGCAGCGACTGGGGTGA---------- : 1435
Hrodentium : GGCACATGCAGCGACTGGGGTGA---------- : 1423
Hpullorum| : GGCACATGCAGC---------- : 1428
Hfennellia : GGCACATGCAGCGACTGGGG---------- : 1445
Htrogontum : GGCACATGCAGCGACTGGGGTG---------- : 1422
Hmuridarum : GGCACATGCAGCGACTGGGG---------- : 1442
Hhepaticus : GNCACATGCAGCGACTGGGGTGA---------- : 1302
Abutzleri| : AGTACATTCAGYGACTGGGG---------- : 1461
Cjejuni|gb : AGTACAATCAGCGACTGGGG---------- : 1458
Wsuccinoge : GGCACATGCAGCGACTGGGG---------- : 1446
ggc a cagcgactgggg

Figure 2 - 45

```
                    *
Hsuis2BXA0  : AACCCGGGCGGC : 1421
Ghominis1|  : ------------ :    -
Ghominis2|  : ------------ :    -
Hfelis|gb|  : ------------ :    -
Hbizzozero  : ------------ :    -
Hbilis|gb|  : ------------ :    -
Hsalomonis  : ------------ :    -
Hpylori|gb  : ------------ :    -
Hcanis|gb|  : ------------ :    -
Hcinaedi|g  : ------------ :    -
Hacinonych  : ------------ :    -
Hnemestrin  : A---------- : 1463
Hcholescys  : ------------ :    -
Hpamatensi  : ------------ :    -
Hmustelae|  : ------------ :    -
Hrodentium  : ------------ :    -
Hpullorum|  : ------------ :    -
Hfennellia  : ------------ :    -
Htrogontum  : ------------ :    -
Hmuridarum  : ------------ :    -
Hhepaticus  : ------------ :    -
Abutzleri|  : ------------ :    -
Cjejuni|gb  : ------------ :    -
Wsuccinoge  : ------------ :    -
```

Figure 2 - 46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95
100
"Candidatus Helicobacter bovis" R2XA
"Helicobacter heilmannii" type 1
"Helicobacter heilmannii" type 2
Helicobacter felis LMG 11750T
Helicobacter bizzozeronii R1051T
Helicobacter salomonis InkinenT
Helicobacter acinonychis LMG 12684T
Helicobacter nemestrinae ATCC 49396T
Helicobacter pylori ATCC 43504
Helicobacter pullorum LMG 16317T
Helicobacter mustelae LMG 18044T
Helicobacter cholecystus R3555T
Helicobacter pametensis M17
Helicobacter muridarum LMG 13646T
Helicobacter hepaticus LMG 16316T
Helicobacter canis LMG 18086T
Helicobacter cinaedi LMG 7545T
Helicobacter bilis gr. 9 ATCC 51630
Helicobacter fennelliae LMG 7546T
Helicobacter trogontum ATCC 700114
Helicobacter rodentium ATCC 700236
Arcobacter butzleri LMG 6620
Campylobacter jejuni LMG 6444T
Wolinella succinogenes LMG 7608T

Fig 3A

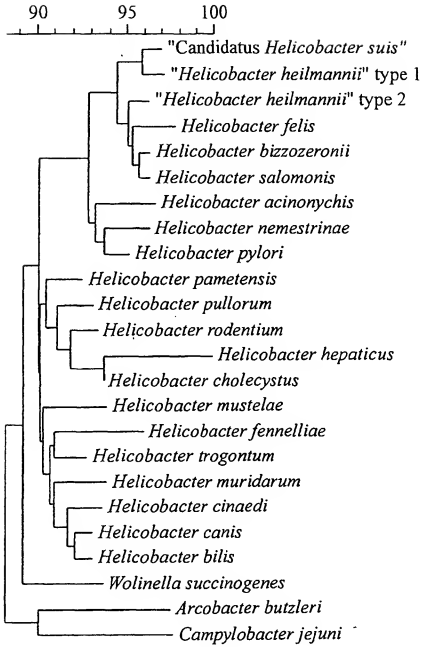

90
95
100
"Candidatus Helicobacter suis"
"Helicobacter heilmannii" type 1
"Helicobacter heilmannii" type 2
Helicobacter felis
Helicobacter bizzozeronii
Helicobacter salomonis
Helicobacter acinonychis
Helicobacter nemestrinae
Helicobacter pylori
Helicobacter pametensis
Helicobacter pullorum
Helicobacter rodentium
Helicobacter hepaticus
Helicobacter cholecystus
Helicobacter mustelae
Helicobacter fennelliae
Helicobacter trogontum
Helicobacter muridarum
Helicobacter cinaedi
Helicobacter canis
Helicobacter bilis
Wolinella succinogenes
Arcobacter butzleri
Campylobacter jejuni

Fig 3B

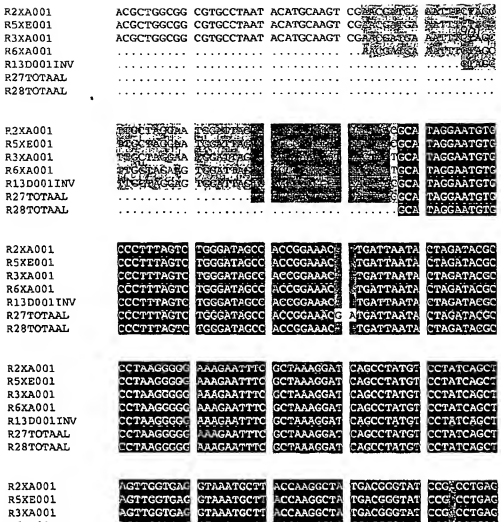


Figure 4 - 1

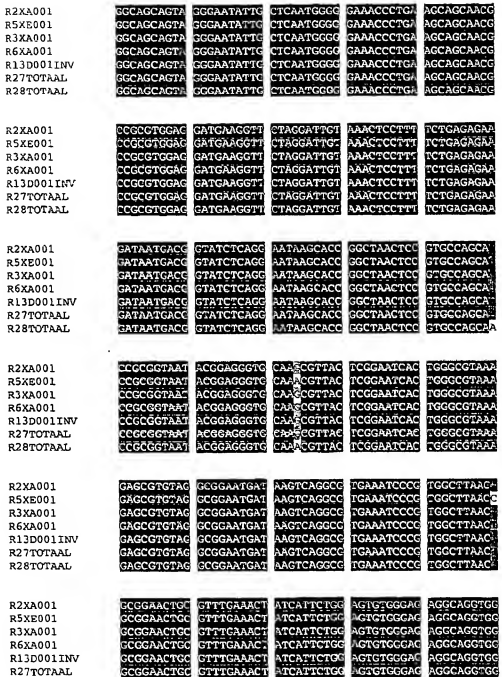
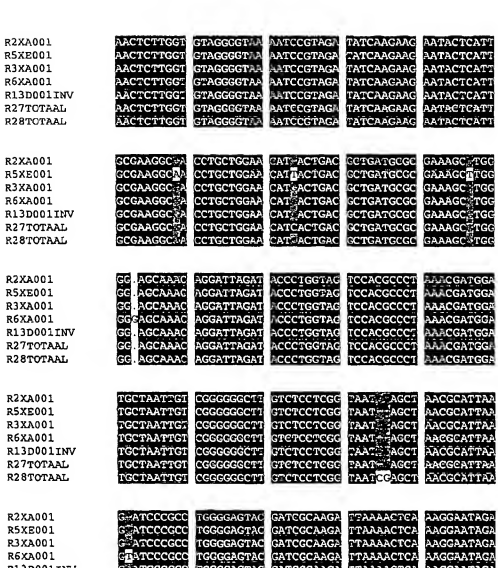

R2XA001
R5XE001
R3XA001
R6XA001
R13D001INV
R27TOTAAL
R28TOTAAL

Figure 4 - 2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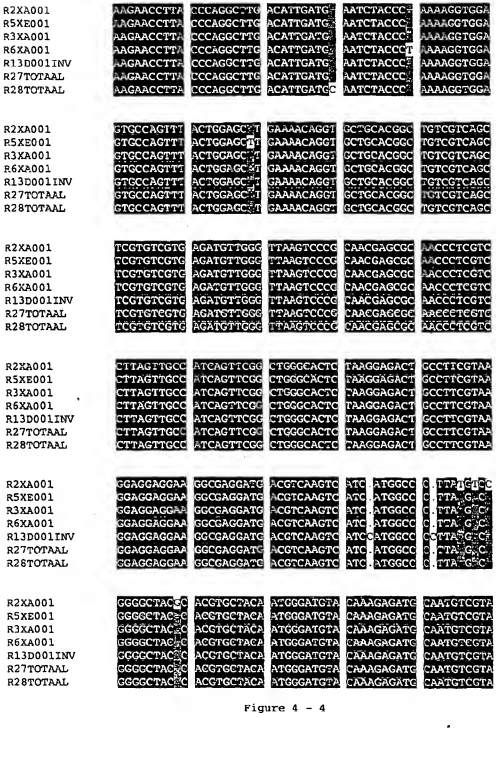
R5XE001
R3XA001
R6XA001
R13D001INV
R27TOTAAL
R28TOTAAL

Figure 4 - 3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R5XE001
R3XA001
R6XA001
R13D001INV
R27TOTAAL
R28TOTAAL

Figure 4 - 4

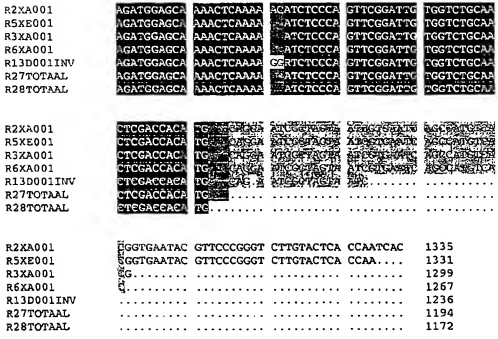

Figure 4 - 5


1 50
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4AXA001 TGCAAGTCGA ACGATGAAGC CTAGCTTGCT AGGTT GTGGCGCACG
6W06001 .... GTGGCGCACG
V14D001 .... GTGGCGCACG
V19DINV001 .... GTGDHGCACG
51 100
2BXA001 GGTGAGTAAT GCATAGATGA CATGCCCTTT AGTTTGGAAT AGCCACTAGA
4AXA001 GGTGAGTAAC GCATAGATGA CATGCCCTTT AGTTTGGAAT AGCCACTAGA
6W06001 GGTGAGTAAT GCATAGATGA CATGCCCTTT AGTTTGGAAT AGCCACTAGA
V14D001 GGTGAGTAAT GCATAGATGA CATGCCCTTT AGTTTGGAAT AGCCACTAGA
V19DINV001 GGTGAGTAAT GCATAGATGA CATGCCCTTT AGTTTGGAAT AGCCACTAGA
101 150
2BXA001 A ATGGTGAT TAATACCAAA TACTACCTTA CGAGGGAAAG ATTTATCGCT
4AXA001 A ATGGTGAT TAATACCAAA TACTACCTTA CGAGGGAAAG ATTTATCGCT
6W06001 A ATGGTGAT TAATACCAAA TACTACCTTA CGAGGGAAAG ATTTATCGCT
V14D001 CCATGGTGAT TAATACCAAA TACTACCTTA CGAGGGAAAG ATTTATCGCT
V19DINV001 C ATGGTGAT TAATACCAAA TACTACCTTA CGAGGGVNAG ATTTATCGCT
151 200
2BXA001 AAAGGATTGC TCTATGTCCT ATCAGCTTGT CGG TGAGGT AAAGGCTCAC
4AXA001 AAAGGATTGC TCTATGTCCT ATCAGCTTGT TGG TGAGGT AAAGGCTCAC
6W06001 AAAGGATTGC TCTATGTCCT ATCAGCTTGT TGG TGAGGT AAAGGCTCAC
V14D001 AAAGGATTGC TCTATGTCCT ATCAGCTTGT TGG TGAGGT AAAGGCTCAC
V19DINV001 AAAGGATTGC TCTATGTCCT ATCAGCTTGT TGGCTGAGGT AAAGGCTCAG
201 250
2BXA001 CAAGG CTAT GACGGGTATC CGGCCTGAGA GGGTGAGCGG ACACACTGGA
4AXA001 CAAGG CTAT GACGGGTATC CGGCCTGAGA GGGTGAGCGG ACACACTGGA
6W06001 CAAGG CTAT GACGGGTATC CGGCCTGAGA GGGTGAGCGG ACACACTGGA
V14D001 CAAGG CTAT GACGGGTATC CGGCCTGAGA GGGTGAGCGG ACACACTGGA
V19DINV001 CAAGGC TAT GACGGGTATC CGGCCTGAGA GGKTGAGCGG ACACACTGGA
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4AXA001 ACTGAGACAC GGTCCAGACT CCTACGGGAG GCAGCAGTAG GGAATATTGC
6W06001 ACTGAGACAC GGTCCAGACT CCTACGGGAG GCAGCAGTAG GGAATATTGC
V14D001 ACTGAGACAC GGTCCAGACT CCTACGGGAG GCAGCAGTAG GGAATATTGC
V19DINV001 ACTGAGACAC GGTCCAGACT CCTACGGGAG GCAGCAGTAG GGAATATTGC
301 350
2BXA001 TCAATGGGGG AAACCCTGA AGCAGCAACG CCGCGTGGAG GATGAAGGTT
4AXA001 TCAATGGGGG AAACCCTGA AGCAGCAACG CCGCGTGGAG GATGAAGGTT
6W06001 TCAATGGGGG AAACCCTGA AGCAGCAACG CCGCGTGGAG GATGAAGGTT
V14D001 TCAATGGGGG AAACCCTGA AGCAGCAACG CCGCGTGGAG GATGAAGGTT
V19DINV001 TCAATGGGGG AAACCCTGA AGCAGCAACG CCGCGTGGAG GATGAAGGTC
351 400
2BXA001 TTAGGATCGT AAACTCCTTT TGTTAGAGAA GATAATGACG GTATCTAACG
4AXA001 TTAGGATCGT AAACTCCTTT TGTTAGAGAA GATAATGACG GTATCTAACG
6W06001 TTAGGATCGT AAACTCCTTT TGTTAGAGAA GATAATGACG GTATCTAACG
V14D001 TTAGGATCGT AAACTCCTTT TGTTAGAGAA GATAATGACG GTATCTAACG
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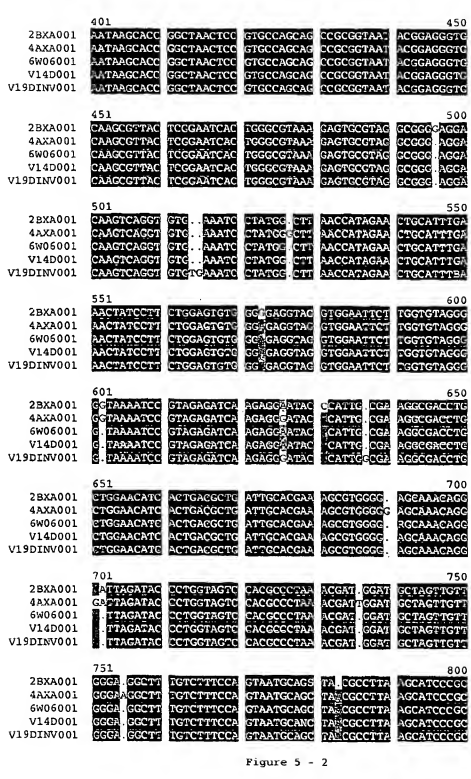
Figure 5 - 1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6W06001 AATAAGCACC GGCTAACTCC GTGCCAGCAG CCGCGGTAAT ACGGAGGGTG
V14D001 AATAAGCACC GGCTAACTCC GTGCCAGCAG CCGCGGTAAT ACGGAGGGTG
V19DINV001 AATAAGCACC GGCTAACTCC GTGCCAGCAG CCGCGGTAAT ACGGAGGGTG
451
500
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4AXA001 CAAGCGTTAC TCGGAATCAC TGGGCGTAAA GAGTGCGTAG GCGGCAAGGA
6W06001 CAAGCGTTAC TCGGAATCAC TGGGCGTAAA GAGTGCGTAG GCGGCAAGGA
V14D001 CAAGCGTTAC TCGGAATCAC TGGGCGTAAA GAGTGCGTAC GCGGCAAGCA
V19DINV001 CAAGCGTTAC TCGGAATCAC TGGGCGTAAA GAGTGCGTAG GCGGCAAGGA
501
550
2BXA001 CAAGTCAGGT GTG..AAATC CTATGG.CTT AACCATAGAA CTGCATTTGA
4AXA001 CAAGTCAGGT GTG..AAATC CTATGG.CTT AACCATAGAA CTGCATTTGA
6W06001 CAAGTCAGGT GTG..AAATC CTATGG.CTT AACCATAGAA CTGCATTTGA
V14D001 CAAGTCAGGT GTG..AAATC CTATGG.CTT AACCATAGAA CTGCATTTGA
V19DINV001 CAAGTCAGGT GTGTGAAATC CTATGG.CTT AACCATAGAA CTGCATTTGA
551
600
2BXA001 AACTATCCTT CTGGAGTGTG GGAGGAGTAC GTGGAATTCT TGGTGTAGGG
4AXA001 AACTATCCTT CTGGAGTGTG GGAGGAGTAC GTGGAATTCT TGGTGTAGGG
6W06001 AACTATCCTT CTGGAGTGTG GCAGGCAGTAC GTGGAATTCT TGGTGTAGGG
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601
650
2BXA001 GGTAAAATCC GTAGAGATCA AGAGGATACC CCATTG.CGA AGGCGACCTG
4AXA001 GGTAAAATCC GTAGAGATCA AGAGGATACC TCATTG.CGA AGGCGACCTG
6W06001 GGTAAAATCC GTAGAGATCA AGAGGATACC TCATTG.CGA AGGCGACCTG
V14D001 GGTAAAATCC GTAGAGATCA AGAGGATACC TCATTG.CGA AGGCGACCTG
V19DINV001 GGTAAAATCC GTAGAGATCA AGAGGATACC TCATTG.CGA AGGCGACCTG
651
700
2BXA001 CTGGAACATC ACTGACGCTG ATTGCACGAA AGCGTGGGGC AGCAAACAGG
4AXA001 CTGGAACATC ACTGACGCTG ATTGCACGAA AGCGTGGGGC AGCAAACAGG
6W06001 CTGGAACATC ACTGACGCTG ATTGCACGAA AGCGTGGGGC AGCAAACAGG
V14D001 CTGGAACATC ACTGACGCTG ATTGCACGAA AGCGTGGGGC AGCAAACAGG
V19DINV001 CTGGAACATC ACTGACGCTG ATTGCACGAA AGCGTGGGGC AGCAAACAGG
701
750
2BXA001 GATTAGATAC CCTGGTAGTC CACGCCCTAA ACGATGCGAT GCTAGTTGTT
4AXA001 GATTAGATAC CCTGGTAGTC CACGCCCTAA ACGATGCGAT GCTAGTTGTT
6W06001 GTTAGATAC CCTGGTAGTC CACGCCCTAA ACGATGCGAT GCTAGTTGTT
V14D001 GTTAGATAC CCTGGTAGTC CACGCCCTAA ACGATGCGAT GCTAGTTGTT
V19DINV001 GTTAGATAC CCTGGTAGTC CACGCCCTAA ACGATGCGAT GCTAGTTGTT
751
800
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4AXA001 GGGATGCCTT TGTCTTTCCA GTAATGCAGC TATGCGCTTA AGCATCCCGC
6W06001 GGGATGCCTT TGTCTTTCCA GTAATGCAGC TATGCGCTTA AGCATCCCGC
V14D001 GGGATGCCTT TGTCTTTCCA GTAATGCANC TATGCGCTTA AGCATCCCGC
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Figure 5 - 2

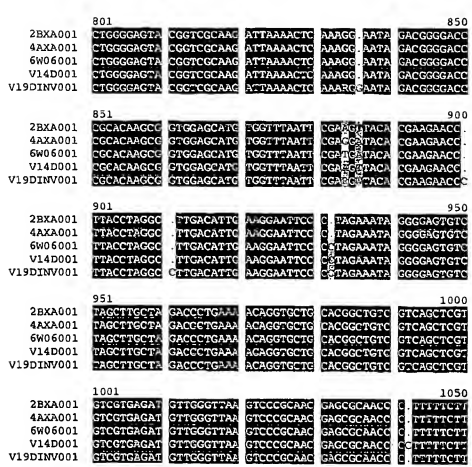
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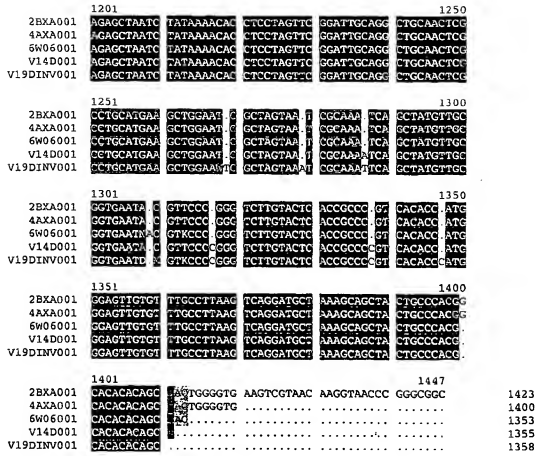
Figure 5 - 3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V14D001 AGAGCTAATG TATAAAACAC CTCCTAGTTC GGATTGCAGG CTGCAACTCC
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V14D001 CCTGCATGAA GCTGGAAT G GCTAGTAA T CGCAAA TCA GCTATGTTGC
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1301 1350
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V19DINV001 CACACACAGC 1358

Figure 5 - 4

European Patent Office

EUROPEAN SEARCH REPORT

Application Number
EP 99 87 0035

DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION
X	PASTER ET AL.: "Phylogeny of Helicobacter felis sp. nov., Helicobacter mustelae, and related bacteria." INTERNATIONAL JOURNAL OF SYSTEMATIC BACTERIOLOGY, vol. 41, no. 1, January 1991 (1991-01), pages 31-38, XP002110981 * the whole document *	1-10	C12Q1/68 A61K31/70
X	BATTLES ET AL.: "Diagnostic assay for helicobacter hepaticus based on nucleotide sequence of its rRNA gene" JOURNAL OF CLINICAL MICROBIOLOGY, vol. 33, no. 5, May 1995 (1995-05), pages 1344-1347, XP002110982 * the whole document *	1-10	
X,D	DEWHIRST F E ET AL: "Phylogeny of Helicobacter isolates from bird and swine feces and description of Helicobacter pametensis sp. nov." INTERNATIONAL JOURNAL OF SYSTEMATIC BACTERIOLOGY, (1994 JUL) 44 (3) 553-60. , XP002110983 * the whole document *	1-10	TECHNICAL FIELDS SEARCHED C12Q
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The present search report has been drawn up for all claims

Place of search	Date of completion of the search	Examiner
THE HAGUE	4 August 1999	Reuter, U

CATEGORY OF CITED DOCUMENTS

X : particularly relevant if taken alone
Y : particularly relevant if combined with another document of the same category
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P : intermediate document

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E : earlier patent document, but published on, or after the filing date
D : document cited in the application
L : document cited for other reasons

& : member of the same patent family, corresponding document

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